

Tue Dec .9 09:26:57 2003

us-09-938-114-3.rpr

Page 5

Search completed: December 8, 2003, 09:55:35
Job time : 6.8 secs

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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:46:14 ; Search time 3.81143 Seconds
(without alignments) 357.812 Million cell updates/sec

Title: US-09-938-114-3
Perfect score: 170
Sequence: 1 DCSDDSSVEGHCYKVKFKOSKWTDAESF 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	138	81.2	117	1	CHB9_CROHO	P81509 crotalus ho
2	133	78.2	146	1	IXB_TRIFL	P23807 trimeresuru
3	131	77.1	123	1	ABA4_TRIAB	P81114 trimeresuru
4	123	72.4	152	1	IXA_TRIFL	P23806 trimeresuru
5	120	70.6	131	1	ABA1_TRIAB	P81111 trimeresuru
6	119	70.0	125	1	BOTB_BOTJA	P22030 bothrops ja
7	117	68.8	133	1	BOTB_BOTJA	P22029 bothrops ja
8	116	68.2	118	1	ABBB_TRIAB	P81116 trimeresuru
9	116	68.2	148	1	CYVB_CRODU	O93427 crotalus du
10	114	67.1	123	1	ECHB_ECHCA	P81996 echis carin
11	113	66.5	125	1	ABA3_TRIAB	P81113 trimeresuru
12	112	65.9	132	1	ABBA_TRIAB	P81115 trimeresuru
13	111	65.3	127	1	CHBA_CROHO	P81508 crotalus ho
14	102.5	60.3	133	1	ECHA_ECHCA	P81017 echis carin
15	100.5	59.1	29	1	MULR_ECHML	P81798 echis multi
16	98	57.6	133	1	RHCA_AGRKH	P81397 agkistrodon
17	96	56.5	135	1	LEGC_CROAT	P21963 crotalus at
18	96	56.5	158	1	CVXA_CRODU	O93426 crotalus du
19	95	55.9	2109	1	PGCA_CHICK	P07898 gallus gall
20	94	55.3	134	1	ABA2_TRIAB	P81112 trimeresuru
21	94	55.3	2415	1	PGCA_HUMAN	P16112 homo sapien
22	92	54.1	2333	1	PGCA_CANFA	Q28343 canis famli
23	92	54.1	2364	1	PGCA_BOVIN	P13608 bos taurus
24	90	52.9	2124	1	PGCA_RAT	P07897 rattus norv
25	90	52.9	2132	1	PGCA_MOUSE	Q61282 mus musculu
26	89	52.4	129	1	RHCB_AGRKH	P81398 agkistrodon
27	84	49.4	158	1	LEGC_TRIST	O9Y9p1 trimeresuru
28	84	49.4	1257	1	PGCN_RAT	P55067 rattus norv
29	84	49.4	1268	1	PGCN_MOUSE	P35066 mus musculu
30	84	49.4	1321	1	PGCN_HUMAN	O4594 homo sapien
31	83	48.8	1458	1	PAZR_FABIT	P49260 oryctolagus
32	82	48.2	883	1	PGCB_MOUSE	Q61361 mus musculu
33	80	47.1	175	1	LITH_BOVIN	P23132 bos taurus

RESULT 1	CHBB_CROHO	STANDARD;	PRT;	117 AA.
ID	CHBB_CROHO	STANDARD;	PRT;	117 AA.
AC	P81509;			
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	CHH-B beta subunit.			
OS	Crotalus horridus horridus (Timber rattlesnake).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;			
OC	Viperidae; Crotalinae; Crotalus.			
OX	NCBI_TaxID=8747;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Venom;			
RC	MEDLINE=96420502; PubMed=8823201;			
RA	Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,			
RA	Smith A.I., Lopez J.A., Berndt M.C.;			
RT	"Binding of a novel 50-kilodalton alphaobagregin from Trimeresurus			
RT	albolabris and related viper venom proteins to the platelet membrane			
RT	glycoprotein Ib-IX-V complex. Effect on platelet aggregation and			
RT	glycoprotein Ib-mediated platelet activation."			
RL	Biochemistry 35:12629-12639(1996).			
CC	!- FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF			
CC	binding, and stimulates agglutination.			
CC	!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- SIMILARITY: Contains 1 C-type lectin family domain.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.			
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.			
KW	Lectin.			
FT	DOMAIN	9	116	C-TYPE LECTIN.
FT	DISULFID	2	13	BY SIMILARITY.
FT	DISULFID	30	115	BY SIMILARITY.
FT	DISULFID	92	92	INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
FT				(POTENTIAL).
FT	DISULFID	95	107	BY SIMILARITY.
SQ	SEQUENCE	117 AA;	13888 MW;	07835BBCB61E9EAD CRC64;

Query Match 81.2%; Score 138; DB 1; Length 117;
Best Local Similarity 75.9%; Pred. No. 1.9e-11;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY	1	DCSSDSSSYEGHCYKVFQSKTWTDAESF	29
Db	1	DCPSDSSSYEGHCYRVFOEWTWDDAEKF	29

RESULT 2					
IXB TRIFL	ID	IXB TRIFL	STANDARD;	PRT;	146 AA.
	AC	P23807; Q91247;			
	DT	01-NOV-1991 (Rel. 20, Created)			
	DT	15-JUL-1998 (Rel. 36, Last sequence update)			

15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
(IX/X-BP).
Trimeresurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
NCBI_TaxID=89087;
[1]
SEQUENCE FROM N.A.
MEDLINE=96184662; PubMed=8645314;
Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
"cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
protein from snake venom.";
Biochem. Biophys. Res. Commun. 220:382-387(1996).
[2]
SEQUENCE OF 24-146.
TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding
protein isolated from the venom of Trimeresurus flavoviridis.
Homology with asialoglycoprotein receptors, proteoglycan core
protein, tetranectin, and lymphocyte Fc epsilon receptor for
immunoglobulin E.";
J. Biol. Chem. 266:14903-14911(1991).
[3]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=9731317; PubMed=9187649;
Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
"Structure of coagulation factors IX/X-binding protein, a heterodimer
of C-type lectin domains.";
Nat. Struct. Biol. 4:438-441(1997).
CC -!- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -!- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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EMBL; D83332; BA011888.1; ..
DR FIR; JC4691; JC4691.
DR PDB; 1LXX; 06-MAY-98.
DR PDB; 1BJ3; 16-AUG-99.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin; Calcium; signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 146 COAGULATION FACTOR IX/FACTOR X-BINDING
FT PROTEIN B CHAIN.
FT DOMAIN 24 144 C-TYPE LECTIN (LONG FORM).
FT DISULFID 25 36 BY SIMILARITY.
FT DISULFID 53 142 BY SIMILARITY.
FT DISULFID 98 98 INTERCHAIN (WITH C-102 OF A CHAIN).
FT DISULFID 119 134 BY SIMILARITY.
FT TURN 27 28
FT STRAND 30 32
FT TURN 33 34
FT STRAND 35 44
FT STRAND 46 54
FT TURN 55 56
FT TURN 58 59

FT STRAND 61 62
FT HELIX 68 82
FT STRAND 86 88
FT TURN 94 97
FT STRAND 100 102
FT TURN 103 104
FT STRAND 113 113
FT STRAND 118 123
FT TURN 124 125
FT STRAND 126 133
FT TURN 134 135
FT STRAND 138 146
SQ SEQUENCE 146 AA; 16922 MW; 8E1961C59F6757C CRC64;
Query Match 78.2%; Score 133; DB 1; Length 146;
Best Local Similarity 72.4%; Pred. No. 1.1e-10;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 DCSSDSSSYEGHCYKVKFKQSKTWTDAESF 29
DB 24 DCPDSSSYEGHCYKVPSEPKNWADAENF 52
RESULT 3
ABA4 TRIAB STANDARD; PRT; 123 AA.
AC P81114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 4.
OS Trimeresurus albobravis (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 1LXX.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
KW Lectin.
FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 119 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBE1219C9B1E CRC64;
Query Match 77.1%; Score 131; DB 1; Length 123;
Best Local Similarity 69.0%; Pred. No. 1.7e-10;
Matches 20; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DCSSDSSSYEGHCYKVKFKQSKTWTDAESF 29
DB 1 DCPDSSSYEGHCYKVPSEPKNWADAENF 29

Tue Dec 9 09:26:57 2003

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Query Match      70.68; Score 120; DB 1; Length 131;
Best Local Similarity 65.5%; Pred. No. 4.9e-09;
Matches 19; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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RESULT 6	BOTB BOTJA	STANDARD;	PRT;	125 AA.
ID	BOTB BOTJA	STANDARD;	PRT;	125 AA.
AC	P22030;			
DT	01-2003-1991 (Rel. 19, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Botrocetin, beta chain (Platelet coagglutinin).			
OS	Bothrops jararaca (Jararaca).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
OC	Viperidae; Crotalinae; Bothrops.			
OX	NCBI_TaxID=8724;			
RN	[1]			
RP	SEQUENCE, AND DISULFIDE BONDS.			
RC	TISSUE=Venom;			
RX	MEDLINE=93157385; PubMed=8430107;			
RA	Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,			
RA	Titani K.;			
RT	"Primary structure of two-chain botrocetin, a von Willebrand factor			
RT	modulator purified from the venom of Bothrops jararaca.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).			
RN	[2]			
RP	SEQUENCE OF 1-40.			
RC	TISSUE=Venom;			
RX	MEDLINE=91129280; PubMed=1993206;			
RA	Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,			
RA	Fukui H., Sugimoto M., Ruggeri Z.M.;			
RT	"Isolation and chemical characterization of two structurally and			
RT	functionally distinct forms of botrocetin, the platelet coagglutinin			
RT	isolated from the venom of Bothrops jararaca.";			
RL	Biochemistry 30:1957-1964(1991).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).			
RX	MEDLINE=22118144; PubMed=12121649;			
RA	Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,			
RA	Liddington R.C.;			
RT	"Structural basis of von Willebrand factor activation by the snake			
RT	toxin botrocetin.";			
RL	Structure 10:943-950(2002).			
CC	!- FUNCTION: Two-chain Botrocetin forms an activated complex with			
CC	vWF, and the complex then binds to platelet GPIb, resulting in			
CC	platelet agglutination.			
CC	!- FUNCTION: There are two distinct forms of the von Willebrand			
CC	factor-dependent platelet coagglutinin. The dimeric form is			
CC	34-times more active than the one-chain Botrocetin in promoting			
CC	vWF binding to platelets.			
CC	!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.			
CC	vWF and Botrocetin form a soluble complex.			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- SIMILARITY: Contains 1 C-type lectin family domain.			
DR	PIR; B47267; B47267.			
DR	PDB; 1IJK; 17-JUL-02.			
DR	PDB; 1FVU; 14-FEB-01.			
DR	InterPro: IPR001304; Lectin.C.			
DR	Pfam: PF00059; lectin c; 1.			
DR	SMART; SM00034; CLECT; 1.			
DR	PROSITE; PS00615; C TYPE LECTIN 1; FALSE_NEG.			
DR	PROSITE; PS50041; C-TYPE_LECTIN_2; 1.			
KW	Lectin; 3D-structure;			
FT	DISULFID 2 13			
FT	DISULFID 30 121			
FT	DISULFID 75 75			
FT	DISULFID 98 113			
FT	INTERCHAIN (WITH C-80 IN ALPHA CHAIN).			

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SQ SEQUENCE      125 AA;   15037 MW;    1ED2027ED817FCA0 CRC64;

Query Match          70.0%; Score 119; DB 1; Length 125;
Best Local Similarity 65.5%; Pred. No. 6.3e-09;
Matches 19; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 1 DCSDDSSSYEGHCYKVFQSKTWTDAESF 29
db 1 DCPDSSSYEGHCYRFFKEWHWDAAEEF 29
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RESULT 7

1	BOTA BOTUA	STANDARD;	PRT;	133 AA.
2	ID	BOTA BOTUA		
3	AC	P22029;		
4	DT	01-AUG-1991 (Rel. 19, Created)		
5	DT	01-JUL-1993 (Rel. 26, Last sequence update)		
6	DT	15-SEP-2003 (Rel. 42, Last annotation update)		
7	DE	Botrocetin, alpha chain (platelet coagglutinin).		
8	OS	Bothrops jararaca (Jararaca).		
9	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
10	OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;		
11	OC	Viperidae; Crotalinae; Bothrops.		
12	OX	NCBI_TaxID=8724;		
13	RN	[1]		
14	RP	SEQUENCE, AND DISULFIDE BONDS.		
15	RC	TISSUE=Venom;		
16	RX	MEDLINE=93157385; PubMed=8430107;		
17	RA	Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,		
18	RA	Titani K.;		
19	RT	"Primary structure of two-chain botrocetin, a von Willebrand factor		
20	RT	modulator purified from the venom of Bothrops jararaca.";		
21	RL	Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).		
22	RN	[2]		
23	RP	SEQUENCE OF 1-40.		
24	RC	TISSUE=Venom;		
25	RX	MEDLINE=91129280; PubMed=1993206;		
26	RA	Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,		
27	RA	Fukui H., Sugimoto M., Ruggeri Z.M.;		
28	RT	"Isolation and chemical characterization of two structurally and		
29	RT	functionally distinct forms of botrocetin, the platelet coagglutinin		
30	RT	isolated from the venom of Bothrops jararaca.";		
31	RL	Biochemistry 30:1957-1964(1991).		
32	RN	[3]		
33	RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).		
34	RX	MEDLINE=22118144; PubMed=12121649;		
35	RA	Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,		
36	RA	Liddington R.C.;		
37	RT	"Structural basis of von Willebrand factor activation by the snake		
38	RT	toxin botrocetin.";		
39	RL	Structure 10:943-950(2002).		
40	CC	-!- FUNCTION: Two-chain Botrocetin forms an activated complex with		
41	CC	vWF, and the complex then binds to platelet GPIb, resulting in		
42	CC	platelet agglutination.		
43	CC	-!- FUNCTION: There are two distinct forms of the von Willebrand		
44	CC	factor-dependent platelet coagglutinin. The dimeric form is		
45	CC	34-times more active than the one-chain Botrocetin in promoting		
46	CC	vWF binding to platelets.		
47	CC	-!- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.		
48	CC	vWF and Botrocetin form a soluble complex.		
49	CC	-!- SUBCELLULAR LOCATION: Secreted.		
50	CC	-!- SIMILARITY: Contains 1 C-type lectin family domain.		
51	DR	PIR; A47267; A47267.		
52	DR	PDB; 1l0K; 17-JUL-02.		
53	DR	PDB; 1fVU; 14-FEB-01.		
54	DR	InterPro; IPR002353; AntifreezeI1.		
55	DR	InterPro; IPR001304; Lectin_C.		
56	DR	Pfam; PF00059; lectin_c; 1.		
57	DR	PRINTS; PR00356; ANTIFREEZEI1.		
58	DR	SMART; SM00034; CLECT; 1.		
59	DR	PROSITE; PS00615; C_TYPE_LECTIN_1; 1.		
60	DR	PROSITE; PS00041; C_TYPE_LECTIN_2; 1.		
61	KW	Lectin; 3D-structure.		

```

FT DISULFID      2   13
FT DISULFID     30  128
FT DISULFID     80   80
FT DISULFID    103  120
SQ SEQUENCE    133 AA; 15215 MW; 54CF4502946AC74B CRC64;

Query Match
Best Local Similarity 68.8%; Score 117; DB 1; Length 133;
Matches 19; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 DCSWSSYEGHCYKVFQSKTWTDAESF 29
    ||| |||||:|||||:|||||
Db 1 DCPGSSYEGNCYKFFQQRWADAERF 29
    ||| |||||:|||||:|||||

RESULT 8
ABBB TRIAB
ID -ABBB TRIAB STANDARD; PRT; 118 AA.
AC P81116;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin B beta subunit.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; IIXX.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN      1  118 C-TYPE LECTIN (LONG FORM).
FT DISULFID    2   13 BY SIMILARITY.
FT DISULFID    75  75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
FT DISULFID    96  111 (BY SIMILARITY).
FT DISULFID   118 AA; 13794 MW; 059EDFF6B474C4CE CRC64;

Query Match
Best Local Similarity 68.2%; Score 116; DB 1; Length 118;
Matches 19; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DCSWSSYEGHCYKVFQSKTWTDAESF 29
    ||| |||||:|||||:|||||
Db 1 DCPGSSYDLYCYKVFQQRWADAERF 29
    ||| |||||:|||||:|||||

RESULT 9
CVXB CRODU
ID -CVXB CRODU STANDARD; PRT; 148 AA.
AC O93427;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Convulxin beta precursor (CVX beta).

```

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OS Crotalus durissus terrificus (South American rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8732;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
RC TISSUE=Venom gland;
RX MEDLINE=98324901; PubMed=9657980;
RA Leduc M., Bon C.;
RT "Cloning of subunits of convulxin, a collagen-like platelet-
RT aggregating protein from Crotalus durissus terrificus venom.";
RL Biochem. J. 333:389-393(1998).
CC -!- FUNCTION: Binds to the platelet and collagen receptor,
CC glycoprotein VI (GPVI).
CC -!- SUBUNIT: Heterohexamer of three alpha chains and three beta
CC chains; disulfide-linked.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y16349; CAA76182.1; -.
DR HSP; P23807; IIXX.
DR InterPro: IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
DR LECTIN; Glycoprotein; Signal.
FT SIGNAL      1   23
FT CHAIN       24  148 CONVULXIN BETA.
FT DOMAIN      34  145 C-TYPE LECTIN.
FT DISULFID    26  26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
FT DISULFID    27  38 (POTENTIAL)
FT DISULFID    55  144 BY SIMILARITY.
FT DISULFID   100  100 BY SIMILARITY.
FT DISULFID   121  136 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
FT DISULFID   148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;
SQ SEQUENCE.

Query Match
Best Local Similarity 68.2%; Score 116; DB 1; Length 148;
Matches 19; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 CSDSWSSYEGHCYKVFQSKTWTDAESF 29
    ||| |||||:|||||:|||||
Db 27 CFSWSSYDRYCYKVFQQRWADAERF 54
    ||| |||||:|||||:|||||

RESULT 10
ECHB ECHCA
ID -ECHB ECHCA STANDARD; PRT; 123 AA.
AC P81996;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Echicetin beta subunit.
OS Echis carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=95091801; PubMed=7999097;

```

RA Peng M., Holt J.C., Niewiarowski S.;
 RT "Isolation, characterization and amino acid sequence of echicetin beta
 RT subunit, a specific inhibitor of von Willebrand factor and thrombin
 RT interaction with glycoprotein Ib.";
 RL Biochem. Biophys. Res. Commun. 205:68-72 (1994).
 RN [2]
 RP SEQUENCE OF 1-30.
 RC TISSUE=Venom;
 RX MEDLINE=97250657; PubMed=9163349;
 RA Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Saqi M.S.A.,
 RA Clemetson K.J.;
 RT "Amino acid sequence of the alpha subunit and computer modelling of
 RT the alpha and beta subunits of echicetin from the venom of Echis
 RT carinatus (saw-scaled viper).";
 RL Biochem. J. 323:533-537 (1997).
 RN [3]
 RP CHARACTERIZATION.
 RC TISSUE=Venom;
 RX MEDLINE=93244424; PubMed=8481512;
 RA Peng M., Lu W., Beviglia L., Niewiarowski S., Kirby E.P.;
 RT "Echicetin: a snake venom protein that inhibits binding of von
 RT Willebrand factor and alboaaggregins to platelet glycoprotein Ib.";
 RL Blood 81:2321-2328 (1993).
 CC -!- FUNCTION: Binds to platelet GPIb and inhibits platelet
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR PIR; JC2415; JC2415.
 DR HSSP; P23807; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 119 BY SIMILARITY.
 FT DISULFID 75 75 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
 FT SIMILARITY).
 FT DISULFID 96 111 BY SIMILARITY.
 SQ SEQUENCE 123 AA; 14869 MW; C42COAD7CDE18CA6 CRC64;
 Query Match 67.1%; Score 114; DB 1; Length 123;
 Best Local Similarity 62.1%; Pred. No. 2.8e-08;
 Matches 18; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DCSDDSSVYEGHCYKVKFQSKTWTDAESF 29
 DB 1 NCLPDSVYEGYCYKVKERNWADAEKF 29
 RESULT 11
 ID AB33 TRIAB STANDARD; PRT; 125 AA.
 AC P8113; 1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaaggregin A subunit 3.
 OS Trimeresurus albobabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=8765;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaaggregins A and B. Structure and interaction with human
 RT platelets.";
 RL Thromb. Haemost. 79:609-613 (1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 79 79 INTERCHAIN (WITH C-75 IN BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 15419 MW; 6PAE64820383F16F CRC64;
 Query Match 65.9%; Score 112; DB 1; Length 132;

RT platelets.";
 RL Thromb. Haemost. 79:609-613 (1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC agglutination.
 CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
 CC disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23807; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 3 123 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 4 15 BY SIMILARITY.
 FT DISULFID 32 121 BY SIMILARITY.
 FT DISULFID 98 113 BY SIMILARITY.
 SQ SEQUENCE 125 AA; 14798 MW; CAFA24C098DF3293 CRC64;
 Query Match 66.5%; Score 113; DB 1; Length 125;
 Best Local Similarity 62.1%; Pred. No. 3.8e-08;
 Matches 18; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DCSDDSSVYEGHCYKVKFQSKTWTDAESF 29
 DB 3 DCPFGSSVYEGYCYKYNKKNWEDAESF 31
 RESULT 12
 ID ABBA TRIAB STANDARD; PRT; 132 AA.
 AC P8115; 1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaaggregin B alpha subunit.
 OS Trimeresurus albobabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Trimeresurus.
 OX NCBI_TaxID=8765;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaaggregins A and B. Structure and interaction with human
 RT platelets.";
 RL Thromb. Haemost. 79:609-613 (1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 79 79 INTERCHAIN (WITH C-75 IN BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 15419 MW; 6PAE64820383F16F CRC64;
 Query Match 65.9%; Score 112; DB 1; Length 132;

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Best Local Similarity 58.6%; Pred. No. 5.5e-08;
Matches 17; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DCSSDSSVEGHCYKVKFQSKTWTDAESF 29
Db 1 DCPDSWSSFKQCYQIVKELKTWDEAXF 29

RESULT 13
CHBA_CROHO
ID CHBA_CROHO STANDARD; PRT; 127 AA.
AC P81508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CHB-B alpha subunit.
OS Crotalus horridus horridus (timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton alphaaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation."
RL Biochemistry 35:12629-12639(1996).
CC -!- FUNCTION: Binds to platelet GPIB/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PROSITE; PS00034; CLECK; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
KW Lectin.
FT DISULFID 11 121 C-TYPE LECTIN.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 120 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-92 IN BETA CHAIN)
FT (POTENTIAL).
FT DISULFID 95 112 BY SIMILARITY.
SQ SEQUENCE 127 AA; 15162 MW; B5DA100D383E3547 CRC64;

Query Match 65.3%; Score 111; DB 1; Length 127;
Best Local Similarity 62.1%; Pred. No. 7.1e-08;
Matches 18; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 DCSSDSSVEGHCYKVKFQSKTWTDAESF 29
Db 3 ECPGWSYDRYCYKFKQEMTWDAERF 31

RESULT 14
ECHA_ECHA
ID ECHA_ECHA STANDARD; PRT; 133 AA.
AC P81017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Echicetin alpha subunit.
OS Echis carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=40353;
RN [1]
RP SEQUENCE.

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RC RX TISSUE=Venom;
RA Polgar J., Magnenat E.M., Peitsch M.C., Wells T.N.C., Sagi M.S.A.,
RA Clemetson K.J.;
RT "Amino acid sequence of the alpha subunit and computer modelling of
RT the alpha and beta subunits of echicetin from the venom of Echis
RT carinatus (saw-scaled viper).";
RL Biochem. J. 323:533-537(1997).
RN [2]
RP CHARACTERIZATION.
RC TISSUE=Venom;
RX MEDLINE=93244424; PubMed=8481512;
RA Peng M., Lu W., Bevilgia L., Niewiarowski S., Kirby E.P.;
RT "Echicetin: a snake venom protein that inhibits binding of von
RT Willebrand factor and alphaaggregins to platelet glycoprotein Ib.";
RL Blood 81:2321-2328(1993).
CC -!- FUNCTION: Binds to platelet GPIb and inhibits platelet
CC agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR HSSP; P23806; I1XX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECK; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 31 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-75 IN BETA CHAIN) (BY
FT SIMILARITY)
SQ SEQUENCE 133 AA; 15803 MW; 8F11C2D0BDC70B16 CRC64;

Query Match 60.3%; Score 102.5; DB 1; Length 133;
Best Local Similarity 58.6%; Pred. No. 9.6e-07;
Matches 17; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 1 DCSSDSSVEGHCYKVKFQSKTWTDAESF 29
Db 3 DCLSGWSFYEGHCYQLFR-LKTWDEAEKY 30

RESULT 15
MULR_ECHML
ID MULR_ECHML STANDARD; PRT; 29 AA.
AC P81798;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Multicativase regulatory subunit (fragment).
OS Echis multisquamatus (Central Asian sand viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
OX NCBI_TaxID=93050;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98104052; PubMed=9443815;
RA Yamada D., Morita T.;
RT "Purification and characterization of a Ca2+ -dependent prothrombin
RT activator, multicativase, from the venom of Echis multisquamatus.";
RL J. Biochem. 122:991-997(1997).
CC -!- FUNCTION: Multicativase, a carinativase-like calcium dependent
CC prothrombin activator, activates prothrombin via recognition of
CC the calcium ion bound conformation of its gamma-carboxyglutamic
CC acid (GLA) domain.
CC -!- DOMAIN: Composed of a catalytic subunit with metalloprotease
CC activity and a regulatory subunit comprising two homologous

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CC      polypeptides bound by S-S bridge(s).
DR      PIR; PC4421; PC4421.
KW      Prothrombin activator; Calcium.
FT      NON_TER 29
SQ      SEQUENCE 29 AA; 3458 MW; DFCA64AD1BC22882 CRC64;

Query Match      59.1%; Score 100.5; DB 1; Length 29;
Best Local Similarity 65.5%; Pred. No. 3.9e-07;
Matches 19; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY      1 DCSSDWSYEGHCYKVFQSKTWTDAESF 29
        |||||
Db       1 DCLPGWSVIEGRICYKVFNQ-KIWKAAEKF 28

Search completed: December 8, 2003, 09:53:10
Job time : 5.14476 secs

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Result No.	Query	Score	Match			DB	ID	Description
			%	Length	No.			
1	163	95.9	152	13	Q9IAM1	Q9iam1	agkistrodon	
2	155	91.2	152	13	Q9DEF9	Q9def9	agkistrodon	
3	155	91.2	152	13	Q8JTW0	Q8jtw0	agkistrodon	
4	148	87.1	146	13	Q8AYA4	Q8aya4	agkistrodon	
5	136	80.0	146	13	Q9IAM0	Q9iam0	agkistrodon	
6	134	78.8	146	13	Q9YI92	Q9yil92	agkistrodon	
7	133	78.2	146	13	Q9DEF8	Q9def8	agkistrodon	
8	133	78.2	146	13	Q8JTV7	Q8jtv7	agkistrodon	
9	132	77.6	124	13	Q9S8M5	Q9s8m5	agkistrodon	
10	132	77.6	146	13	Q8JTW1	Q8jtw1	agkistrodon	
11	127	74.7	146	13	Q9DG31	Q9dg31	agkistrodon	
12	124	72.9	146	13	Q9I840	Q9i840	agkistrodon	
13	124	72.9	155	13	Q8JTV8	Q8jtv8	agkistrodon	
14	123	72.4	131	13	Q9PSM9	Q9psm9	echis carin	
15	123	72.4	146	13	Q9BUU0	Q9buu0	trimeresur	
16	121	71.2	124	13	Q9OWL9	Q9owl9	agkistrodon	

DR PROSITE; PS00615; C_TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16726 MW; 7360B6D6964131BB CRC64;

Query Match 80.0%; Score 136; DB 13; Length 146;
Best Local Similarity 75.9%; Pred. No. 1e-11;
Matches 22; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DCSDDSSSYEGHCYKVKFKQSKTWTDAESF 29
||| ||||| ||||| ||| ||| ||| |||
Db 24 DCPDSSSYEGHCYKVPDEPKTWADAEPF 52

RESULT 6
Q9YI92 PRELIMINARY; PRT; 146 AA.
ID Q9YI92
AC Q9YI92;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mamushigin baly.
OS Agkistrodon halys blomhoffi (Mamushi) (Gloydus blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=61300;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98319530; PubMed=9657448;
RA Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,
RA Suzuki M., Matsui T., Titani K., Yoshioka A.;
RT "The cDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
halys blomhoffii venom.";
RL Thromb. Haemost. 79:1199-1207(1998).
DR EMBL; AB019616; BAA34425.1; -.
DR HSP; P23807; IIXX.
DR Interpro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE LECTIN_2; 1.
SQ SEQUENCE 146 AA; 17064 MW; 9EDA84BCC24E76D CRC64;

Query Match 78.8%; Score 134; DB 13; Length 146;
Best Local Similarity 72.4%; Pred. No. 1.9e-11;
Matches 21; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DCSDDSSSYEGHCYKVKFKQSKTWTDAESF 29
||| ||||| ||||| ||| ||| ||| |||
Db 24 DCPDSSSYEGHCYKVPDEPKTWADAEPF 52

RESULT 7
Q9DEF8 PRELIMINARY; PRT; 146 AA.
ID Q9DEF8
AC Q9DEF8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anticoagulant protein-B precursor.
GN ACP-B.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y.,
RA Chang C., Shimohigashi Y., Ohno M.;
RT "Purification, sequencing, and cDNA cloning of a heterodimeric

QX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Zha X., Xu K.;
 RL SUBMITTED (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF350324; AAK26430.1; -
 DR HSP; P23807; IIXX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 124 AA; 14701 MW; 4682D5E80CB3DC518 CRC64;

 Query Match 77.6%; Score 132; DB 13; Length 124;
 Best Local Similarity 72.4%; Pred. No. 3.1e-11;
 Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 DCSDDSSSYEGHCYKVFQSKTWTDAESF 29
 Db 2 DCPSEWSSYEGHCYKPFNPENLKNWDAENF 30

 RESULT 10
 Q8JWI1 PRELIMINARY; PRT; 146 AA.
 AC Q8JWI1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Agkisacutacin B-chain.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Sceleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yu H., Xiang K., Wang Y., Liu J.;
 RT "B chain of agkisacutacin from Deinagkistrodon acutus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091756; AAM22785.1; -
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR003990; Pancreatiss_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSA.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 SQ SEQUENCE 146 AA; 16740 MW; 6260B6D68741317C CRC64;

 Query Match 77.6%; Score 132; DB 13; Length 146;
 Best Local Similarity 72.4%; Pred. No. 3.7e-11;
 Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

 Qy 1 DCSDDSSSYEGHCYKVFQSKTWTDAESF 29
 Db 24 DCPSEWSSYEGHCYKPFNPENLKNWDAENF 52

 RESULT 11
 Q9DG31 PRELIMINARY; PRT; 146 AA.
 AC Q9DG31;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Halysin B-chain precursor.
 OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Sceleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Agkistrodon.

Qy	1	DCSDWSSYEGHCYKVFQSKTWTDAESF	29
		:	
Db	24	DCPSGWSYEGHCYKFPNEKNWADAERF	52

RESULT 13			
Q8JTV8		PRELIMINARY;	PRT; 155 AA.
ID	Q8JTV8		
AC	Q8JTV8;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	C-type lectin.		
OS	Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Crotalinae; Deinagkistrodon.		
NCBI_TaxID=36307;			
NCBI_TaxID=36307;			
SEQUENCE FROM N.A.			
Yu H., Xiang K., Wang Y., Liu J.;			
RA	"Member of C-type lectin family from Deinagkistrodon acutus.";		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
ENBL; AY019760; AAM22788.1; -			
DR	InterPro: IPR001304; Lectin_C.		
DR	InterPro: IPR001390; Pancratis_ac.		
DR	Pfam: PF00059; lectin_c; 1.		
DR	PRINTS; PR01504; PNCREATITSAP.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.		
DR	PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.		
KW	Lectin.		
SEQUENCE	155 AA; 17944 MW; 3E935FF53773AB94	CRC64;	
Query Match	72.9%;	Score 124; DB 13; Length 155;	
Best Local Similarity	69.0%;	Pred. No. 5.5e-10;	
Matches	20; Conservative	2; Mismatches	7; Indels 0;

Qy	1	DCSDWSSYEGHCYKVFQSKTWTDAESF	29
Db	24	DCPSGWSYEGHCYQVFSDLKNWDDAESF	52

RESULT 14			
Q9PSM9		PRELIMINARY;	PRT; 131 AA.
ID	Q9PSM9		
AC	Q9PSM9;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	ECLV IX/X-RP alpha SUBUNIT-COAGULATION factor IX/factor X-binding protein alpha subunit.		
DE	Echis carinatus (Saw-scaled viper).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Viperinae; Echis.		
NCBI_TaxID=40353;			
NCBI_TaxID=40353;			
SEQUENCE			
Medline=96196635; PubMed=8611513;			
Chen Y.L., Tsai I.H.;			
RA	"Functional and sequence characterization of coagulation factor IX/factor X-binding protein from the venom of Echis carinatus leucogaster.";		
RL	Biochemistry 35:5264-5271 (1996).		
DR	HSP; P23806; IIXX.		
DR	InterPro; IPR001304; Lectin_C.		
DR	Pfam; PF00059; lectin_c; 1.		
DR	SMART; SM00034; CLECT; 1.		
DR	PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.		
DR	PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.		
SEQUENCE	131 AA; 15439 MW; B85E6C5CBF317E24	CRC64;	

```

Query Match          72.4%; Score 123; DB 13; Length 131;
Best Local Similarity 69.0%; Pred. No. 6.4e-10;
Matches 20; Conservative 2; Mismatches 7; Indels 0; Gaps

Qy 1 DCSSDWSYEGHCYKVFQSKTWTDAESF 29
Db 1 DCLPGWSSHEGHCHYKVFNEYTKWDAEF 29
      ||| :||||| : |||||
      ||| :||||| : |||||

RESULT 15
Q98UJ0 PRELIMINARY; PRT; 146 AA.
AC Q98UJ0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Factor XI/factor X binding protein A chain.
GN XI/XSP-A.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
ON [1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshimaru M., Chijiwa T.,
RT Chang C., Fukumaki Y., Ohno M.;
RT "Characterization and molecular evolution of an anticoagulant protein
RT from Agkistrodon actus venom.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046491; BAB21452.1; -.
DR HSSP; P23806; 11XX.
DR InterPro; IPR001304; Lectin C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16461 MW; 6ADF0E032544316C CRC64;

Query Match          72.4%; Score 123; DB 13; Length 146;
Best Local Similarity 74.1%; Pred. No. 7.2e-10;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps

Qy 1 DCSSDWSYEGHCYKVFQSKTWTDAE 27
Db 18 DCLSGWSYEGHCYKAFKFKTWEDAE 44
      ||| :||||| : |||||
      ||| :||||| : |||||

Search completed: December 8, 2003, 09:54:48
Job time : 14.0857 secs

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Search completed: December 8, 2003, 09:54:48
Job time : 14.0857 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:34:19 : Search time 751.514 Seconds
(without alignments)
937.879 Million cell updates/sec

Title: US-09-938-114-3

Perfect score: 170

Sequence: 1 DCSDSWSSYEGCHVKYFKQSKTWTDAESF 29

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US0938114/runat_08122003_091000_22859/app_query.fasta_1.725
-DB=EST -QPM=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0938114 @CGN 1.1 4382 @runat_08122003_091000_22859 -NCFU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estli.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_pbg.*
27: em_gss_vrl.*
28: gb_gesl.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	133	78.2	172	12	BM401696	BM401696 PHIA01F S
2	127	74.7	378	12	BM401618	BM401618 JLIAC07F S
3	127	74.7	391	12	BM401469	BM401469 JHLE03F S
4	127	74.7	475	12	BM401621	BM401621 JLIID02F S
5	127	74.7	504	12	BM401628	BM401628 JLIIE12F S
6	127	74.7	510	12	BM401667	BM401667 JLIIE12F S
7	127	74.7	512	12	BM401495	BM401495 JH2H07F S
8	121	71.2	343	12	BM401656	BM401656 JH2B09F S
9	120	70.6	633	12	BM401686	BM401686 JH2E04F S
10	119	70.0	378	12	BM401686	BM401686 PHO15FB S
11	119	70.0	574	12	BM401620	BM401620 JLI1C11F S
12	119	70.0	654	12	BM401417	BM401417 GH061F S
13	117	68.8	301	12	BM401401	BM401401 GH025F S
14	115	67.6	460	12	BM401654	BM401654 JH2D07F S
15	112	65.9	374	12	BM401460	BM401460 JH1D06F S
16	112	65.9	497	12	BM401520	BM401520 JH2G02F S
17	100	58.8	406	12	BM401552	BM401552 JH3E12F S
18	99	58.2	618	12	BM401598	BM401598 JH4F11F S
19	98	57.6	200	12	BM401682	BM401682 PHO12F S
20	97	57.1	743	14	CD099404	BM401669 JH2H09F S
21	95	55.9	729	13	BU255510	CD099404 AGENCOURT
22	95	55.9	763	13	BU255510	BU255510 603744951
23	95	55.9	765	13	BU400634	BU408882 602955211
24	95	55.9	796	13	BU250042	BU400634 604137678
25	95	55.9	846	13	BU410105	BU250042 603403475
26	95	55.9	951	13	BU409519	BU410105 603158654
27	95	55.9	967	13	BU314865	BU409519 603159673
28	95	55.9	1022	13	BU127176	BU314865 603487735
29	94	55.3	389	12	BG897747	BU127176 603115043
30	94	55.3	389	12	BG897804	BG897747 HOA25-1-A
31	94	55.3	426	12	BG901081	BG897804 HOA25-1-H
32	94	55.3	498	10	BE550485	BG901081 HOA53-1-E
33	94	55.3	598	12	BG899799	BE550485 7A27b11.X
34	94	55.3	644	12	BG899799	BG899799 HOA40-1-A
35	94	55.3	681	29	AG094039	BG899799 HOA39-1-H
36	94	55.3	706	12	BG329062	AG094039 Pan crogl
37	94	55.3	708	9	AI907207	BG329062 HNC11-1-A
38	94	55.3	708	12	BG925582	AI907207 RC-BT133-
39	94	55.3	723	12	BG925582	BG925582 HNC30-1-C
40	94	55.3	750	12	BG913209	BG925582 HNC59-1-E
41	91	53.5	598	13	BU323232	BG913209 602811871
42	91	53.5	702	13	BU266055	BU323232 603490804
43	91	53.5	703	13	BU269611	BU266055 603815327
44	91	53.5	726	13	BU230613	BU269611 603816223
45	91	53.5	727	13	BU360029	BU230613 603399651
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ALIGNMENTS

RESULT 1
BM401696
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM401696 172 bp mRNA linear EST 01-MAY-2002
PHIA01F Snake Bothrops insularis library IL2 Bothrops insularis
CDNA 5', similar to Snake venom C-type lectin, mRNA sequence.

BM401696
EST.

Bothrops insularis (island jataraca)

Bothrops insularis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 172)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..172
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 34 a 39 c 47 g 42 t 10 others
 ORIGIN

Alignment Scores:
 Pred. No.: 1.35e-09 Length: 172
 Score: 133.00 Matches: 21
 Percent Similarity: 79.31% Conservative: 2
 Best Local Similarity: 72.41% Mismatches: 6
 Query Match: 78.24% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401696 (1-172)

Qy 1 AspCysSerSerAspTTPSerSerTyGluGlyHisCysTyLysValPheLysGlnSer 20
 |||||
 Db 82 GATTGTCCCTCTGATGTGTCCTCCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 141
 |||||

Qy 21 LysThrTrpThrAspAlaGluSerPhe 29
 |||||
 Db 142 ATGACTGGCGGATGACAGAGATT 168
 |||||

RESULT 2
 BM401618
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401618 378 bp mRNA linear EST 01-MAY-2002
 JLIC07F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401618 GI:20376246
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 378)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..378
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 88 a 91 c 102 g 95 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3.12e-08 Length: 378
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401618 (1-378)

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 |||||
 Db 78 GATTGTCCCTCTGATGTGTCCTCCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 137
 |||||

Qy 21 LysThrTrpThrAspAlaGluSer 28
 |||||
 Db 138 ATGACTGGCGGATGACAGAGAT 161
 |||||

RESULT 3
 BM401469
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401469 391 bp mRNA linear EST 01-MAY-2002
 JHLE09F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401469 GI:20376097
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 391)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)
 22347338
 12459276
 Contact: Paulo Lee Ho
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
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 Location/Qualifiers
 1..378
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
 RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
 venom glands were primed with oligo-(dT) and reverse
 transcribed to cDNA using Superscript Plasmid System for
 cDNA Synthesis and Cloning (Life Technologies). The cDNAs
 were selected by size (350-600 pb and up 600 pb) in
 agarose gel electrophoresis, linked to Eco RI adapters and
 directionally cloned in pGEM11zf+ vector (Promega). ESTs
 were generated from random clones and grouped in unique
 sequences. The putative identification of each EST or
 cluster was obtained through Blast searches (e-value <
 e-05)."

BASE COUNT 88 a 91 c 102 g 95 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3.12e-08 Length: 378
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401618 (1-378)

Qy 1 AspCysSerSerAspTTPSerSerTyGluGlyHisCysTyLysValPheLysGlnSer 20
 |||||
 Db 78 GATTGTCCCTCTGATGTGTCCTCCCTATGAGGGCATTGCTACAGCTCTTCAACACGG 137
 |||||

Qy 21 LysThrTrpThrAspAlaGluSer 28
 |||||
 Db 138 ATGACTGGCGGATGACAGAGAT 161
 |||||

RESULT 3
 BM401469
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM401469 391 bp mRNA linear EST 01-MAY-2002
 JHLE09F Snake Bothrops insularis library IL3 Bothrops insularis
 cDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 BM401469 GI:20376097
 EST.
 Bothrops insularis (island jararaca)
 Bothrops insularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 391)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of
 the pitviper snake Bothrops insularis through the generation of
 expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

MEDLINE
12459276
PUBMED
COMMENT

Contact: Paulo Lee Ho
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Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL03A (see Reference)
Seq primer: M13F.

FEATURES

source

Location/Qualifiers

1. .391
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 91 a 92 c 113 g 95 t

ORIGIN

Alignment Scores:
Pred. No.: 3.28e-08 Length: 475
Score: 127.00 Matches: 20
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 6
Query Match: 74.71% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401469 (1-391)

QY 1 AspCysSerSerAspTrpSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
Db 135 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAGCTCTTTCAACACG 194
QY 21 LysThrTrpThrAspAlaGluSer 28
Db 195 ATGAACCTGGCGGATGCAGAGAT 218

RESULT 4

BM401621

LOCUS

DEFINITION

JL1D02F Snake Bothrops insularis library IL3 Bothrops insularis

CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Bothrops insularis (Island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 475)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED

COMMENT

Contact: Paulo Lee Ho

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Tel: 55 11 37 26 7222 ext. 2083

Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13F.

FEATURES

source

Location/Qualifiers

1. .475
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 113 a 111 c 133 g 117 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 4.38e-08 Length: 475
Score: 127.00 Matches: 20
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 6
Query Match: 74.71% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401621 (1-475)

QY 1 AspCysSerSerAspTrpSerTyrrGluGlyHisCysTyrrLysValPheLysGlnSer 20
Db 129 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAGCTCTTTCAACACG 188
QY 21 LysThrTrpThrAspAlaGluSer 28
Db 189 ATGAACCTGGCGGATGCAGAGAT 212

RESULT 5

BM401628

LOCUS

DEFINITION

JL1E12F Snake Bothrops insularis library IL3 Bothrops insularis

CDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Bothrops insularis (Island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 504)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED

COMMENT

Contact: Paulo Lee Ho

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Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

source
 Location/Qualifiers
 1. 504
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"

/tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 128 a 113 c 140 g 120 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4.79e-08 Length: 504
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401628 (1-504)

Qy 1 AspCysSerSerAspTrpSerSerTyGluGlyHisCysTyLysValPheLysGlnSer 20
 Db 96 GATTGTCCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAAGCTCTTCAAAACACGG 155

Qy 21 LysThrTrpThrAspAlaGluSer 28
 Db 156 ATGAACCTGGCGGATGCAGAGAAT 179

RESULT 6
 BM401667
 LOCUS J12H07F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401667.1 GI:20376295
 VERSION EST.
 KEYWORDS Bothrops insularis (island jararaca)
 SOURCE Bothrops insularis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 REFERENCE 1 (bases 1 to 510)
 Junqueira-de-Azevedo, J.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 12459276
 PUBMED 12459276
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br

CONTACT: Paulo Lee Ho
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 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

source
 Location/Qualifiers
 1. 510
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"

/tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 128 a 117 c 141 g 121 t 3 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4.87e-08 Length: 510
 Score: 127.00 Matches: 20
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 6
 Query Match: 74.71% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401667 (1-510)

Qy 1 AspCysSerSerAspTrpSerSerTyGluGlyHisCysTyLysValPheLysGlnSer 20
 Db 93 GATTGTCCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAAGCTCTTCAAAACACGG 152

Qy 21 LysThrTrpThrAspAlaGluSer 28
 Db 153 ATGAACCTGGCGGATGCAGAGAAT 176

RESULT 7
 BM401495
 LOCUS JH2B09F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401495.1 GI:20376123
 VERSION EST.
 KEYWORDS Bothrops insularis (island jararaca)
 SOURCE Bothrops insularis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 REFERENCE 1 (bases 1 to 512)
 Junqueira-de-Azevedo, J.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 12459276
 PUBMED 12459276
 COMMENT Contact: Paulo Lee Ho
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 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
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CONTACT: Paulo Lee Ho
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 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.
 Location/Qualifiers


```

source
1. .512
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

BASE COUNT 129 a 116 c 143 g 119 t 5 others
ORIGIN

Alignment Scores:
Pred. No.: 4.9e-08 Length: 512
Score: 127.00 Matches: 20
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 6
Query Match: 74.71% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401495 (1-512)

QY 1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrIysValPheLysGlnSer 20
|||||
Db 99 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGTACAAAGCTCTTCAACAACG 158
QY 21 LysThrTrpThrAspAlaGluSer 28
|||||
Db 159 ATGAACCTGGCGGATGCAGAGAT 192

RESULT 8
BM401656
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BM401656 343 bp mRNA linear EST 01-MAY-2002
JL2E04F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
BM401656 GI:20376284
Bothrops insularis (island jararaca)
Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 343)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
22347338
12459276
Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13F.

FEATURES
source
1. .343
/organism="Bothrops insularis"
/mol_type="mRNA"

```

source
1. .512
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

BASE COUNT 79 a 83 c 90 g 86 t 5 others
ORIGIN

Alignment Scores:
Pred. No.: 1.93e-07 Length: 343
Score: 121.00 Matches: 19
Percent Similarity: 76.92% Conservative: 1
Best Local Similarity: 73.08% Mismatches: 6
Query Match: 71.18% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401656 (1-343)

QY 1 AspCysSerSerAspTrpSerSerTyrGluGlyHisCysTyrIysValPheLysGlnSer 20
|||||
Db 131 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGTACAAAGCTCTTCAACAACG 190
QY 21 LysThrTrpThrAspAla 26
|||||
Db 191 ATGAACCTGGCGGATGCA 208

RESULT 9
BM401686
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

BM401686 633 bp mRNA linear EST 01-MAY-2002
PH015FB Snake Bothrops insularis library IL2 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
BM401686 GI:20376314
Bothrops insularis (island jararaca)
Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
1 (bases 1 to 633)
Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
Gene 299 (1-2), 279-291 (2002)
22347338
12459276
Contact: Paulo Lee Ho
Centro de Biotecnologia
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Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL02A (see Reference)
Seq primer: M13F.

FEATURES
Location/Qualifiers
1. .633
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dt) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 145 a 148 c 155 g 171 t 14 others
ORIGIN

Alignment Scores:
Pred. No.: 6.69e-07 Length: 633
Score: 120.00 Matches: 19
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 67.86% Mismatches: 7
Query Match: 70.59% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401686 (1-633)

Qy 1 AspCysSerSerAspTrpSerSerTyrgluGlyHisCysTyrlsValPheLysGlnSer 20
|||||
Db 82 GATTGTCCCTCTGATTGGTCCCTCTATGGAGGCAATTGCTACAGCTCTTCAACACGG 141
|||||
Qy 21 LysThrTrpThrAspAlaGluSer 28
|||||
Db 142 ATGAACCTGGCGGATGCAGAGAT 165
|||||

RESULT 10
BM401620
LOCUS BM401620 378 bp mRNA linear EST 01-MAY-2002
DEFINITION J11C11F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401620
VERSION BM401620.1 GI:20376248
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)
ORGANISM Bothrops insularis

REFERENCE 1 (bases 1 to 378)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br

This EST corresponds to cluster BIT11A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1..378
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dt) and reverse

FEATURES
source

transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 82 a 105 c 99 g 92 t
ORIGIN

Alignment Scores:
Pred. No.: 4.31e-07 Length: 378
Score: 119.00 Matches: 19
Percent Similarity: 72.41% Conservative: 2
Best Local Similarity: 65.52% Mismatches: 8
Query Match: 70.00% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401620 (1-378)

Qy 1 AspCysSerSerAspTrpSerSerTyrgluGlyHisCysTyrlsValPheLysGlnSer 20
|||||
Db 149 GATTGTCCCTCTGATTGGTCCCTCTATGAAGGAGTTGCTACAGGCTCTTCAACAAAAG 208
|||||
Qy 21 LysThrTrpThrAspAlaGluSerPhe 29
|||||
Db 209 ATGAACCTGGCGGATGCAGAGAAATTC 235
|||||

RESULT 11
BM401417

LOCUS BM401417 574 bp mRNA linear EST 01-MAY-2002
DEFINITION GH061F Snake Bothrops insularis library IL2 Bothrops insularis cDNA
5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401417
VERSION BM401417.1 GI:20376045
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)
ORGANISM Bothrops insularis

REFERENCE 1 (bases 1 to 574)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br

This EST corresponds to cluster BIT10A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1..574
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dt) and reverse
transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in

FEATURES
source


```

BASE COUNT      63 a    78 c    86 g    74 t
ORIGIN

Alignment Scores:
Pred. No.:      5.92e-07      Length:      301
Score:          117.00      Matches:      19
Percent Similarity: 78.57%      Conservative: 3
Best Local Similarity: 67.86%      Mismatches: 6
Query Match:     68.82%      Indels:      0
DB:              12      Gaps:      0

US-09-938-114-3 (1-29) x BM401654 (1-301)

QY 2 CysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSerLys 21
   |||
Db 87 TGTCCTTGGGTGGTCTCTCTATGATGAGCAATGCTACAGGGTCTTCAAGGAACCTCAA 146
   |||

QY 22 ThrTrpThrAspAlaGluSerPhe 29
   |||
Db 147 ACTGGGATGATGCAGAGAGTTTC 170
   |||

RESULT 14
BM401460
LOCUS
DEFINITION
  JH1D06F Snake Bothrops insularis library IL3 Bothrops insularis
  cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
  BM401460
VERSION
  BM401460.1 GI:20376088
KEYWORDS
  EST.
SOURCE
  Bothrops insularis (island jararaca)
ORGANISM
  Bothrops insularis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
  Viperidae; Crotalinae; Bothrops.
REFERENCE
  1 (bases 1 to 460)
  Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
  A survey of gene expression and diversity in the venom glands of
  the pitviper snake Bothrops insularis through the generation of
  expressed sequence tags (ESTs)
  Gene 299 (1-2), 279-291 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12459276
COMMENT
  Contact: Paulo Lee Ho
  Instituto Butantan
  Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
  Tel: 55 11 37 26 7222 ext. 2083
  Fax: 55 11 37 26 1505
  Email: hoplee@usp.br
  This EST corresponds to cluster BITL13A (see Reference)
  Seq primer: M13F.
  Location/Qualifiers
    source
      1..460
        /organism="Bothrops insularis"
        /mol_type="mRNA"
        /db_xref="taxon:8723"
        /tissue_type="venom glands"
        /clone_lib="Snake Bothrops insularis library IL3"
        /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
        RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
        venom glands were primed with oligo-(dT) and reverse
        transcribed to cDNA using Superscript Plasmid System for
        cDNA Synthesis and Cloning (Life Technologies). The cDNAs
        were selected by size (350-600 pb and up 600 pb) in
        agarose gel electrophoresis, linked to Eco RI adapters and
        directionally cloned in pGEM11zf+ vector (Promega). ESTs
        were generated from random clones and grouped in unique
        sequences. The putative identification of each EST or
        cluster was obtained through Blast searches (e-value <
        e-05)."
```

```

BASE COUNT      106 a    106 c    145 g    103 t
ORIGIN
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```

Alignment Scores:
Pred. No.:      2.15e-06      Length:      460
Score:          115.00      Matches:      18
Percent Similarity: 72.41%      Conservative: 3
Best Local Similarity: 62.07%      Mismatches: 8
Query Match:     67.65%      Indels:      0
DB:              12      Gaps:      0

US-09-938-114-3 (1-29) x BM401460 (1-460)

QY 1 AspCysSerSerAspTrpSerTyrGluGlyHisCysTyrLysValPheLysGlnSer 20
   |||
Db 143 GATTGTCCCTCTGTTGGTCTCTCTATGAAGGAGTTGCTACAGGGTCTTCACTGAACCG 202
   |||

QY 21 LysThrTrpThrAspAlaGluSerPhe 29
   |||
Db 203 CAAAGCTGGGCCGATGCAGAGAGTTTC 229
   |||

RESULT 15
BM401520
LOCUS
DEFINITION
  JH2G02F Snake Bothrops insularis library IL3 Bothrops insularis
  cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION
  BM401520
VERSION
  BM401520.1 GI:20376148
KEYWORDS
  EST.
SOURCE
  Bothrops insularis (island jararaca)
ORGANISM
  Bothrops insularis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
  Viperidae; Crotalinae; Bothrops.
REFERENCE
  1 (bases 1 to 374)
  Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
  A survey of gene expression and diversity in the venom glands of
  the pitviper snake Bothrops insularis through the generation of
  expressed sequence tags (ESTs)
  Gene 299 (1-2), 279-291 (2002)
JOURNAL
  MEDLINE
  PUBMED
  12459276
COMMENT
  Contact: Paulo Lee Ho
  Centro de Biotecnologia
  Instituto Butantan
  Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
  Tel: 55 11 37 26 7222 ext. 2083
  Fax: 55 11 37 26 1505
  Email: hoplee@usp.br
  This EST corresponds to cluster BITL06A (see Reference)
  Seq primer: M13F.
  Location/Qualifiers
    source
      1..374
        /organism="Bothrops insularis"
        /mol_type="mRNA"
        /db_xref="taxon:8723"
        /tissue_type="venom glands"
        /clone_lib="Snake Bothrops insularis library IL3"
        /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
        RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
        venom glands were primed with oligo-(dT) and reverse
        transcribed to cDNA using Superscript Plasmid System for
        cDNA Synthesis and Cloning (Life Technologies). The cDNAs
        were selected by size (350-600 pb and up 600 pb) in
        agarose gel electrophoresis, linked to Eco RI adapters and
        directionally cloned in pGEM11zf+ vector (Promega). ESTs
        were generated from random clones and grouped in unique
        sequences. The putative identification of each EST or
        cluster was obtained through Blast searches (e-value <
        e-05)."
```

```

BASE COUNT      83 a    83 c    114 g    94 t
ORIGIN

Alignment Scores:
Pred. No.:      4.22e-06      Length:      374
Score:          112.00      Matches:      18
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Percent Similarity: 74.07% Conservative: 2
Best Local Similarity: 66.67% Mismatches: 7
Query Match: 65.88% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-3 (1-29) x BM401520 (1-374)

QY 1 AspCysSerSerAspTyrSerSerTyGluGlyHisCysTyrLysValPheLysGlnSer 20
Db 130 GATTGTCCCTGATTGGTCTCTATGAGGGAGTTGCTACAAGCTCTTCAGACAAGAG 189

QY 21 LysThrTrpThrAspAlaGlu 27

Db 190 TTGAAGTGGGAGGATGCAGAG 210

Search completed: December 8, 2003, 17:24:33
Job time : 754.514 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:45:44 ; Search time 10.2 Seconds
(without alignments)
284.544 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYEGFCVKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	93.5	146	24	ABU08799
2	95	88.0	120	23	ABH83143
3	94	87.0	30	22	AAW51540
4	94	87.0	146	22	AAW51544
5	86	79.6	21	16	AAW71980
6	86	79.6	28	13	AAK23886
7	86	79.6	116	13	AAK24427
8	86	79.6	123	14	AAK38225
9	84	77.8	30	16	AAW72232

10	84	77.8	32	16	AAW72231	Vipera palestinae
11	84	77.8	43	16	AAW72234	Vipera palestinae
12	84	77.8	50	13	AAW23889	N-terminal sequenc
13	84	77.8	52	16	AAW72233	Vipera palestinae
14	84	77.8	127	16	AAW72236	Vipera palestinae
15	84	77.8	132	16	AAW72235	Vipera palestinae
16	84	77.8	145	23	AAO14521	Korean adder snake
17	83	76.9	36	13	AAW23885	N-terminal sequenc
18	83	76.9	38	16	AAW71978	Snake venom derive
19	83	76.9	110	23	AAO20975	110-mer central lo
20	83	76.9	126	16	AAW71979	Snake venom derive
21	83	76.9	126	21	AAW5627	Snake venom derive
22	83	76.9	126	23	AAO20973	126-mer wild-type
23	83	76.9	126	23	AAO20980	M7-G4 K20A mutant
24	83	76.9	126	23	AAO20981	M8-G4 D54A mutant
25	83	76.9	126	23	AAO20982	M9-G4 Y58A mutant
26	83	76.9	126	23	AAO20983	M10-G4 K61A mutant
27	83	76.9	126	23	AAO20984	M11-G4 E62A mutant
28	83	76.9	126	23	AAO20985	M12-G4 Y63A mutant
29	83	76.9	126	23	AAO20986	M13-G4 R66A mutant
30	83	76.9	126	23	AAO20987	M14-G4 Y67A mutant
31	83	76.9	126	23	AAO20988	M15-G4 R100A mutant
32	83	76.9	126	23	AAO20989	M16-G4 D101A mutant
33	83	76.9	126	23	AAO20990	M17-G4 R103A mutant
34	83	76.9	126	23	AAO20991	M18-G4 R105A mutant
35	83	76.9	126	23	AAO20992	M19-G4 E106A mutant
36	83	76.9	126	23	AAO20993	M20-G4 F108A mutant
37	83	76.9	126	23	AAO20994	M21-G4 D54A, D101N
38	83	76.9	126	23	AAO20995	M22-G4 D54A, D101A
39	83	76.9	126	23	AAO20996	M23-G4 D54N, D101A
40	83	76.9	126	23	AAO20997	M24-G4 D54A, D101A
41	83	76.9	126	23	AAO20998	M25-G4 D101A, E106
42	83	76.9	126	23	AAO20999	M26-G4 D101A, E106
43	83	76.9	127	13	AAW24426	Sequence of the pl
44	83	76.9	149	16	AAW71981	Snake venom antith
45	83	76.9	149	21	AAW5628	Snake venom derive

ALIGNMENTS

RESULT 1

ABU08799
ID ABU08799 standard; Protein; 146 AA.

XX ABU08799;

XX AC

XX 02-JUN-2003 (first entry)

XX DE

XX Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX Antithrombosis; beta chain; fibrin hydrolysis; blood clot; enzyme;
XX platelet aggregation; vaso-occlusive disorder; thromboembolic disorder;
XX myocardial infarction; restenosis; cancer; neurodegenerative disease;
XX angioathic thrombosis; cerebral thrombosis; thromboangiitis obliterans;
XX ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
XX unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
XX peripheral arterial occlusion; stroke; atherosclerosis; inflammation;
XX thrombosis.

XX OS Deinagkistrodon acutus.

XX FH

XX Key Location/Qualifiers

XX Peptide 1..23

XX Protein /note= "Leader peptide"

XX /note= "Mature antithrombosis enzyme beta chain. Residues 24 to 40 specifically claimed in claim 8"

XX Misc-difference 72

XX /label= Unknown

XX Misc-difference 72

XX /note= "Encoded by TNN"

XX /label= Unknown

```

FT Misc-difference 72 /note= "Encoded by NNN"
FT FT /label= Unknown
FT /note= "Encoded by NNN"
FT Misc-difference 72 /label= Unknown
FT /note= "Encoded by NNT"
XX
XX US6489451-B1.
XX
XX 03-DEC-2002.
XX
XX 10-APR-1998; 98US-0058740.
XX
XX 10-APR-1997; 97US-043886P.
XX (HEFE-) HEFEI SIU FUNG USFC PHARM CO LTD.
XX
XX Li BX, Cheng X;
XX
XX WPI; 2003-352116/33.
XX N-PSDB; ABX93674.
XX
XX New purified Agkistrodon actus anti-thrombosis enzyme, useful for
XX preventing and treating vaso-occlusive and thromboembolic disorders,
XX including myocardial infarction, restenosis, cerebral thrombosis and
XX unstable angina
XX
XX Disclosure; Fig 1; 19pp; English.
XX
XX The invention relates to a new Deinagkistrodon actus anti-thrombosis
XX enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and
XX prevents platelet aggregation. The anti-thrombosis enzyme was
XX administered to rabbits intravenously. Thrombosis was determined before
XX and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the
XX Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour
XX following administration at 0.005 micro/kg and this activity was
XX increased significantly at 1.0 hour and at 0.01 micro /kg. The
XX composition is useful for preventing and treating vaso-occlusive and
XX thromboembolic disorders, including myocardial infarction, restenosis,
XX angioathic thrombosis, cerebral thrombosis, ischaemic cerebral vascular
XX diseases, unstable angina, acute thrombosis, unstable stenocardia,
XX thromboangitis obliterans, pulmonary embolism, deep vein thrombosis,
XX peripheral arterial occlusion, stroke. It is also useful for treating
XX atherosclerosis, oedema and inflammation, cancer and neurodegenerative
XX diseases. The present sequence represents the amino acid sequence of the
XX Deinagkistrodon actus antithrombosis enzyme beta chain.
XX
XX Sequence 146 AA;
XX
XX Query Match 93.5%; Score 101; DB 24; Length 146;
XX Best Local Similarity 94.1%; Pred. No. 2.2e-06;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 DCPSEWSYEGFCYKPF 17
XX |||||:|||||
XX 24 DCPSEWSYEGHCYKPF 40
XX
XX RESULT 2
XX ABB83143
XX ID ABB83143 standard; protein; 120 AA.
XX
XX AC ABB83143;
XX
XX DT 06-AUG-2002 (first entry)
XX
XX DE Ahylysantinfarctase thrombase II subunit B.
XX
XX Ahylysantinfarctase thrombase II subunit B; snake; venom;
XX Chinese Agkistrodon acutus; purification.
XX
XX Agkistrodon acutus.
XX
XX Query Match 88.0%; Score 95; DB 23; Length 120;
XX Best Local Similarity 82.4%; Pred. No. 1.2e-05;
XX Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 DCPSEWSYEGFCYKPF 17
XX |||||:|||||
XX Db 1 DCPSDWSYDHCYKPF 17
XX
XX RESULT 3
XX AAM51540
XX ID AAM51540 standard; peptide; 30 AA.
XX
XX AC AAM51540;
XX
XX DT 10-JAN-2002 (first entry)
XX
XX DE Snake venom blood anticoagulant peptide #1.
XX
XX KW Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
XX thrombosis.
XX
XX OS Agkistrodon halyx.
XX
XX KR2001049671-A.
XX 15-JUN-2001.
XX
XX 29-JUN-2000; 2000KR-0036591.
XX
XX 29-JUN-1999; 99KR-0025105.
XX
XX (BIOB-) BIOBUD CO LTD.
XX
XX Jang YS, Jung GH, Kim DS, Koo BH, Son YD;
XX WPI; 2001-637330/73.
XX
XX Halyxin as blood anticoagulation protein separated from snake venom -
XX Example 1; Page 8; 21pp; Korean.
XX
XX The invention relates to halyxin, a novel protein with very strong
XX blood anticoagulation activity. The protein was separated from snake

```


CC venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
 CC be used in the treatment of thrombogenesis. The present sequence is
 CC a peptide derived from the protein.

XX SQ Sequence 30 AA;

Query Match 87.0%; Score 94; DB 22; Length 30;

Best Local Similarity 88.2%; Pred. No. 4.9e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

DB 1 DCPSGWSSYEGHCYKPF 17

RESULT 4

AAAM51544
 ID AAM51544 standard; Protein; 146 AA.

XX AC AAM51544;

XX DT 10-JAN-2002 (first entry)

XX DE Snake venom blood anticoagulant halyxin B chain.

XX KW Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
 XX KW thrombosis.

XX OS Agkistrodon halys.

XX PN KR2001049671-A.

XX PD 15-JUN-2001.

XX PF 29-JUN-2000; 2000KR-0036591.

XX PR 29-JUN-1999; 99KR-0025105.

XX PA (BIOB-) BIOUD CO LTD.

XX PI Jang YS, Jung GH, Kim DS, Koo BH, Son YD;

XX DR WPI; 2001-637330/73.

XX DR N-PSDB; AAI71877.

XX PT Halyxin as blood anticoagulation protein separated from snake venom -

XX PS Claim 2; Page 11-12; 21pp; Korean.

XX CC The invention relates to halyxin, a novel protein with very strong
 CC blood anticoagulation activity. The protein was separated from snake
 CC venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can
 CC be used in the treatment of thrombogenesis. The present sequence
 CC is the B chain of halyxin.

XX SQ Sequence 146 AA;

Query Match 87.0%; Score 94; DB 22; Length 146;

Best Local Similarity 88.2%; Pred. No. 2e-05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

DB 24 DCPSGWSSYEGHCYKPF 40

RESULT 5

AAAR71980

ID AAR71980 standard; peptide; 21 AA.

XX AC AAR71980;

XX DT 25-MAR-2003 (updated)

DT 28-NOV-1995 (first entry)
 XX Snake venom derived antithrombotic peptide.

XX KW Antithrombotic peptide; snake venom; platelet binding inhibition;
 XX OS von Willebrand factors; Crotales horridus horridus.

XX PN Crotales horridus horridus.

XX WO9508573-A1.

XX PD 30-MAR-1995.

XX PF 21-SEP-1994; 94WO-JP01555.

XX PR 22-SEP-1993; 93JP-0236975.

XX PA (AJIN) AJINOMOTO KK.

XX PI Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;

XX PI Tanaka A, Yamamoto H, Yoshimoto R;

XX DR WPI; 1995-139559/18.

XX PT Single-chain antithrombotic peptide - obtained by cleaving an
 XX PT oligopeptide from snake venom to break inter-chain di:sulphide
 XX PT bonds but preserve intra-chain di:sulphide bonds

XX PS Example 2; Page 45; 84pp; Japanese.

XX CC AAR71980 is a snake venom derived antithrombotic peptide, prepared
 XX CC by cleaving the interpeptide but retaining the intrapeptide
 XX CC disulphide bonds of the original snake venom oligopeptide. The
 XX CC peptide has the advantage of avoiding significant thrombocytopenia
 XX CC when administered at the minimum dose, for in vivo inhibition of
 XX CC platelet von Willebrand factor binding.
 XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 21 AA;

Query Match 79.6%; Score 86; DB 16; Length 21;

Best Local Similarity 76.5%; Pred. No. 4.4e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

DB 1 DCPSDWSSYEGHCYRVF 17

RESULT 6

AAAR23886

ID AAR23886 standard; Protein; 28 AA.

XX AC AAR23886;

XX DT 25-MAR-2003 (updated)

XX DT 21-NOV-1992 (first entry)

XX DE N-terminal sequence of the earlier eluting subunit (CH-B-beta) of
 XX DE the later eluting peak of the platelet antiadhesive peptide (PAA).

XX KW Platelet adherence inhibitor; platelet anti-adhesive;

XX KW antithrombotic agent; von Willebrand Factor;

XX KW platelet glycoprotein GPIb-IX complex.

XX OS Crotales horridus horridus.

XX WO9208472-A1.

XX PD 29-MAY-1992.

XX PF 14-NOV-1991; 91WO-US08516.

PR 16-NOV-1990; 90US-0614443.
 XX (CORT-) COR THERAPEUTICS INC.
 XX Scarborough RM;
 XX WPI; 1992-199936/24.
 XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 PT inhibit thrombus formation; for treatment of arteriosclerosis,
 PT atherosclerosis, acute myocardial infarction, chronic unstable
 PT angina, etc.
 XX
 PS Claim 4; Page 30; 5pp; English.
 XX
 CC The PAA was purified from a solution of snake venom. Analysis of
 CC the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins
 CC migrating with a mol. wt. 23-28 kD. Both were able to inhibit
 CC botrocetin and ristocetin induced platelet agglutination. They were
 CC called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta)
 CC and later eluting subunit (CHH-B-alpha) were individually submitted
 CC to N-terminal sequence analysis. The complete amino acid sequence
 CC for the alpha and beta chains are given in AAR24426 and AAR24427.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 28 AA;
 Query Match 79.6%; Score 86; DB 13; Length 28;
 Best Local Similarity 76.5%; Pred. No. 5.7e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 DB 1 DCPSDWSSYEGHCYRVF 17
 RESULT 7
 AAR24427
 ID AAR24427 standard; Protein; 116 AA.
 XX
 AC AAR24427;
 XX
 XX 25-MAR-2003 (updated)
 DT 21-NOV-1992 (first entry)
 XX
 XX Sequence of the platelet glycoprotein GPIb inhibitor beta chain
 DE (CHH-B-beta).
 XX
 XX Platelet adherence inhibitor; platelet anti-adhesive;
 KW antithrombotic agent; von Willebrand Factor;
 KW platelet glycoprotein GPIb-IX complex.
 XX
 OS Crotalus horridus horridus.
 XX
 XX WO9208472-A1.
 FN 29-MAY-1992.
 XX
 PD 14-NOV-1991; 91WO-US08516.
 XX
 PF 16-NOV-1990; 90US-0614443.
 XX
 XX (CORT-) COR THERAPEUTICS INC.
 XX Scarborough RM;
 XX WPI; 1992-199936/24.
 XX
 XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 XX inhibit thrombus formation; for treatment of arteriosclerosis,
 XX atherosclerosis, acute myocardial infarction, chronic unstable
 XX angina, etc.
 XX
 PS Example; Fig 6; 5pp; English.

XX
 CC The PAA was purified from a solution of snake venom. Analysis of
 CC the peak inhibitory fractions by SDS-PAGE revealed 2 major proteins
 CC migrating with a mol. wt. 23-28 kD. Both were able to inhibit
 CC botrocetin and ristocetin induced platelet agglutination. They were
 CC called CHH-A and CHH-B. The earlier eluting subunit (CHH-B-beta)
 CC and later eluting subunit (CHH-B-alpha) were individually submitted
 CC to N-terminal sequence analysis. The complete amino acid sequence
 CC for the alpha and beta chains are given in AAR24426 and AAR24427.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 116 AA;
 Query Match 79.6%; Score 86; DB 13; Length 116;
 Best Local Similarity 76.5%; Pred. No. 0.00021;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 DB 1 DCPSDWSSYEGHCYRVF 17

RESULT 8

AAR38225
 ID AAR38225 standard; protein; 123 AA.

XX
 AC AAR38225;
 XX
 XX 25-MAR-2003 (updated)
 DT 01-OCT-1993 (first entry)
 XX
 XX Sequence of polypeptide chain of alboaagregin A (AL-A).
 DE
 XX
 KW Venom; snake; platelet-binding protein.
 XX
 XX Trimeresurus albolabris.
 OS
 XX WO9311151-A1.
 FN 10-JUN-1993.
 PD
 XX 01-DEC-1992; 92WO-US10344.
 PF
 XX 03-DEC-1991; 91US-0803630.
 PR
 XX 05-JUN-1992; 92US-0893929.
 XX
 XX (UTEM) UNIV TEMPLE.
 XX
 XX Kirby EP, Peng M;
 XX WPI; 1993-196991/24.
 XX
 XX New platelet-binding proteins obtained from snake venom - inhibit
 PT binding of von Willebrand factor to platelet membrane
 PT glycoprotein IB, useful in therapy, diagnosis and surgery
 XX
 XX Claim 4; Page 47; 74pp; English.

XX
 CC AL-A may be obtd. from snake venom. It has a mol. wt. of about 45
 CC kDa. AL-A contains two types of polypeptide chains, with mol. wt. of
 CC about 18 kDa and about 15 kDa, respectively. Each of these two types
 CC of chains is actually composed of two subtypes. Thus, AL-A comprises
 CC four non-identical polypeptide chains. A possible variation of
 CC AAR38224 has been found, characterised by Asp at posn. three in lieu
 CC of Cys.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 123 AA;
 Query Match 79.6%; Score 86; DB 14; Length 123;
 Best Local Similarity 76.5%; Pred. No. 0.00022;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||
 Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 9
 AAR72232
 ID AAR72232 standard; peptide; 30 AA.

AC AAR72232;
 XX
 XX 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)
 XX

DE Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;
 KW platelet binding; von Willebrand factor.

XX Vipera palestinae.

OS WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

XX WPI; 1995-147392/19.

XX Peptide derived from Vipera palestinae venom - inhibits binding

PT of platelets to von Willebrand factor, useful as antithrombotic

PT agent

XX Claim 3; Page 17; 37pp; Japanese.

XX AAR72232 is a Vipera palestinae venom derived N-terminal fragment,

CC the full peptide is given in AAR72236. A peptide compsn. comprising

CC AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets

CC to von Willebrand factors and can therefore be used as an anti-

CC thrombotic agent.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 30 AA;

XX Query Match 77.8%; Score 84; DB 16; Length 30;

XX Best Local Similarity 76.5%; Pred. No. 0.00011;

XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 10
 AAR72231

ID AAR72231 standard; peptide; 32 AA.

XX AAR72231;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

DE Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

Query Match 77.8%; Score 84; DB 16; Length 32;

Best Local Similarity 76.5%; Pred. No. 0.00012;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHCYKVF 19

RESULT 11
 AAR72234

ID AAR72234 standard; peptide; 43 AA.

XX AAR72234;

XX 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX Vipera palestinae venom derived peptide N-terminal fragment.

XX Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;

XX platelet binding; von Willebrand factor.

OS Vipera palestinae.

XX WO9509183-A1.

PN 06-APR-1995.

XX 27-SEP-1994; 94WO-JP01583.

XX 28-SEP-1993; 93JP-0241666.

PR 14-JAN-1994; 94JP-0002691.

PR 10-JUN-1994; 94JP-0128518.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kaide K, Kobayashi T;

PI

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||:|||||

Db 3 DCPSDWSSYEGHC

XX WPI; 1995-147392/19.
 XX Peptide derived from Vipera palestinae venom - inhibits binding
 PT of platelets to von Willebrand factor, useful as antithrombotic
 agent
 XX Claim 4; Page 18; 37pp; Japanese.
 XX AAR72234 is a Vipera palestinae venom derived N-terminal fragment,
 CC the full peptide is given in AAR72236. A peptide compsn. comprising
 CC AAR72236 and AAR72235 is claimed, it inhibits the binding of platelets
 CC to von Willebrand factors and can therefore be used as an anti-
 CC thrombotic agent.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 43 AA;
 Query Match 77.8%; Score 84; DB 16; Length 43;
 Best Local Similarity 76.5%; Pred. No. 0.00016;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKVP 17
 Db 1 DCPSDWSSHEGHCYKVF 17
 RESULT 12
 AAR23889
 ID AAR23889 standard; Protein; 50 AA.
 XX AAR23889;
 XX 25-MAR-2003 (updated)
 DT 21-NOV-1992 (first entry)
 XX N-terminal sequence of the earlier eluting subunit PP-beta of
 DE the later eluting peak of the platelet antiadhesive peptide (PAA).
 XX Platelet adherence inhibitor; platelet anti-adhesive;
 KW antithrombotic agent; von Willebrand Factor;
 KW platelet glycoprotein GPIb-IX complex.
 XX Pseudocerastes persicus.
 XX WO9208472-A1.
 XX 29-MAY-1992.
 XX 14-NOV-1991; 91WO-US08516.
 XX 16-NOV-1990; 90US-0614443.
 XX (CORT-) COR THERAPEUTICS INC.
 XX Scarborough RM;
 XX WPI; 1992-199936/24.
 XX Platelet antiadhesive peptide(s) obtd. from snake venom - also
 PT inhibit thrombus formation; for treatment of arteriosclerosis,
 PT atherosclerosis, acute myocardial infarction, chronic unstable
 PT angina, etc.
 XX Claim 7; Page 30; 5pp; English.
 XX The PAA was purified from a solution of snake venom. The earlier
 CC eluting subunit, PP-beta was subjected to Edman degradation for 50
 CC cycles to obtain the sequence in AAR23889. The later eluting
 CC sequence - the PP-alpha chain was determined for 31 cycles to give
 CC the SQ in AAR23890.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 50 AA;
 Query Match 77.8%; Score 84; DB 13; Length 50;
 Best Local Similarity 76.5%; Pred. No. 0.00018;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKVP 17
 Db 1 DCPSDWSSHEGHCYKVF 17
 RESULT 13
 AAR72233
 ID AAR72233 standard; peptide; 52 AA.
 XX AAR72233;
 XX 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)
 XX Vipera palestinae venom derived peptide N-terminal fragment.
 DE Vipera palestinae; venom; N-terminal fragment; antithrombotic agent;
 KW platelet binding; von Willebrand factor.
 XX Vipera palestinae.
 OS WO9509183-A1.
 XX 06-APR-1995.
 PD 27-SEP-1994; 94WO-JP01583.
 PP 28-SEP-1993; 93JP-0241666.
 PR 14-JAN-1994; 94JP-0002691.
 PR 10-JUN-1994; 94JP-0128518.
 XX (AJIN) AJINOMOTO KK.
 XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
 XX WPI; 1995-147392/19.
 XX Peptide derived from Vipera palestinae venom - inhibits binding
 PT of platelets to von Willebrand factor, useful as antithrombotic
 agent
 XX Claim 4; Page 18; 37pp; Japanese.
 XX AAR72233 is a Vipera palestinae venom derived N-terminal fragment,
 CC the full peptide is given in AAR72235. A peptide compsn. comprising
 CC AAR72235 and AAR72236 is claimed, it inhibits the binding of platelets
 CC to von Willebrand factors and can therefore be used as an anti-
 CC thrombotic agent.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 52 AA;
 Query Match 77.8%; Score 84; DB 16; Length 52;
 Best Local Similarity 76.5%; Pred. No. 0.00019;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKVP 17
 Db 3 DCPSDWSSHEGHCYKVF 19
 RESULT 14
 AAR72236
 ID AAR72236 standard; peptide; 127 AA.
 XX AAR72236;
 XX

```

DT 25-MAR-2003 (updated)
DT 04-DEC-1995 (first entry)
DE Vipera palestinae venom derived peptide.
XX
XX Vipera palestinae; venom; antithrombotic agent;
KW platelet binding; von Willebrand factor.
XX
OS Vipera palestinae.
XX
XX WO9509183-A1.
XX
XX 06-APR-1995.
XX
XX 27-SEP-1994; 94WO-JP01583.
XX
XX 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Pages 19-20; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 127 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 127;
XX Best Local Similarity 76.5%; Pred. No. 0.00043;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
1 DCPSDWSHSHGHCYKVF 17

RESULT 15
ID AAR72235
XX AAR72235 standard; peptide; 132 AA.
XX
XX AC AAR72235;
XX
XX 25-MAR-2003 (updated)
DT 04-DEC-1995 (first entry)
XX
DE Vipera palestinae venom derived peptide.
XX
XX Vipera palestinae; venom; antithrombotic agent;
KW platelet binding; von Willebrand factor.
XX
XX Vipera palestinae.
XX
XX WO9509183-A1.
XX
XX 06-APR-1995.
XX
XX 27-SEP-1994; 94WO-JP01583.
XX
XX 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Pages 19-20; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 132 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 132;
XX Best Local Similarity 76.5%; Pred. No. 0.00044;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
3 DCPSDWSHSHGHCYKVF 19

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Job time : 10.2 secs

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PR 10-JUN-1994; 94JP-0128518.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Fukuchi N, Ishii K, Kaida K, Kobayashi T;
XX WPI; 1995-147392/19.
XX
XX Peptide derived from Vipera palestinae venom - inhibits binding
XX of platelets to von Willebrand factor, useful as antithrombotic
XX agent
XX
XX Claim 5; Page 19; 37pp; Japanese.
XX
XX AAR72235 is a Vipera palestinae venom derived peptide. A peptide
XX compen. comprising AAR72235 and AAR72236 is claimed, it inhibits the
XX binding of platelets to von Willebrand factors and can therefore
XX be used as an anti- thrombotic agent.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 132 AA;
XX
XX Query Match 77.8%; Score 84; DB 16; Length 132;
XX Best Local Similarity 76.5%; Pred. No. 0.00044;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db ||||:||||:||||
3 DCPSDWSHSHGHCYKVF 19

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Search completed: December 8, 2003, 09:52:34
Job time : 10.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:50:40 ; Search time 3.69143 Seconds
(without alignments)
194.853 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSSYEGFCVKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	17	4	US-09-058-740-4
2	86	79.6	21	2	US-08-612-840A-3
3	86	79.6	117	1	US-07-614-443A-2
4	86	79.6	117	1	US-08-294-859-2
5	86	79.6	117	1	US-08-481-676-2
6	86	79.6	123	1	US-07-893-929A-4
7	86	79.6	123	5	PCT-US92-10344-4
8	84	77.8	50	1	US-07-614-443A-5
9	84	77.8	50	1	US-08-294-859-5
10	84	77.8	50	1	US-08-481-676-5
11	83	76.9	38	2	US-08-612-840A-1
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16	83	76.9	149	2	US-08-612-840A-8
17	81	75.0	29	4	US-09-058-740-3
18	81	75.0	129	4	US-09-058-740-2
19	80	74.1	107	1	US-07-893-929A-6
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22	80	74.1	128	5	PCT-US92-10344-8
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24	79	73.1	131	5	PCT-US92-10344-1
25	74	68.5	125	1	US-07-893-929A-3
26	74	68.5	125	5	PCT-US92-10344-3
27	69	63.9	130	1	US-07-893-929A-7

28 69 63.9 130 5 PCT-US92-10344-7 Sequence 7, Appli
29 69 63.9 132 1 US-07-893-929A-5 Sequence 5, Appli
30 69 63.9 132 5 PCT-US92-10344-5 Sequence 5, Appli
31 68 63.0 15 1 US-08-551-128A-1 Sequence 1, Appli
32 67 62.0 123 1 US-07-893-929A-10 Sequence 10, Appli
33 67 62.0 123 5 PCT-US92-10344-10 Sequence 10, Appli
34 65 60.2 30 2 US-08-894-403-3 Sequence 3, Appli
35 64 59.3 22 1 US-07-614-443A-7 Sequence 7, Appli
36 64 59.3 22 1 US-08-294-859-7 Sequence 7, Appli
37 64 59.3 22 1 US-08-481-676-7 Sequence 7, Appli
38 64 59.3 133 1 US-07-893-929A-9 Sequence 9, Appli
39 64 59.3 133 5 PCT-US92-10344-9 Sequence 9, Appli
40 61 56.5 15 1 US-08-551-128A-2 Sequence 2, Appli
41 60 55.6 20 1 US-07-614-443A-4 Sequence 4, Appli
42 60 55.6 20 1 US-08-294-859-4 Sequence 4, Appli
43 60 55.6 20 1 US-08-481-676-4 Sequence 4, Appli
44 60 55.6 30 2 US-08-894-403-4 Sequence 4, Appli
45 59 54.6 31 1 US-07-614-443A-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
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; Sequence 4, Application US/09058740
; Patent NO. 6489451
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Rong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,740
; FILING DATE: 10-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-058-740-4

Query Match 100.0%; Score 108; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
| | | | | | | | | | | | | | | | | | |
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 2

US-08-612-840A-3
; Sequence 3, Application US/08612840A
; Patent No. 5856126

GENERAL INFORMATION:

APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Obion, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5856126man F. Oblon

REGISTRATION NUMBER: 24,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-612-840A-3

Query Match 79.6%; Score 86; DB 2; Length 21;
Best Local Similarity 76.5%; Pred. No. 6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 3

US-07-614-443A-2

; Sequence 2, Application US/07614443A
; Patent No. 5342830

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/614,443A
FILING DATE: 19901116
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22803-20003.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-614-443A-2

Query Match 79.6%; Score 86; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 3.5e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 4

US-08-294-859-2
; Sequence 2, Application US/08294859
; Patent No. 5679542

GENERAL INFORMATION:

APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,859
FILING DATE: 29-AUG-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-294-859-2

Query Match 79.6%; Score 86; DB 1; Length 117;
 Best Local Similarity 76.5%; Pred. No. 3.5e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPSDWSSYEGHCYRVF 17

RESULT 5

US-08-481-676-2
 Sequence 2, Application US/08481676
 Patent No. 5744584
 GENERAL INFORMATION:
 APPLICANT: SCARBOROUGH, ROBERT M.
 TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,676
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/294,859
 FILING DATE: 29-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2803-0003.10
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-481-676-2

Query Match 79.6%; Score 86; DB 1; Length 117;
 Best Local Similarity 76.5%; Pred. No. 3.5e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPSDWSSYEGHCYRVF 17

RESULT 6

US-07-893-929A-4

Sequence 4, Application US/07893929A
 Patent No. 5336667
 GENERAL INFORMATION:
 APPLICANT: Kirby, Edward P.
 APPLICANT: Peng, Man-ling
 TITLE OF INVENTION: Alboaggregins: Platelet
 TITLE OF INVENTION: Agonists Which Bind To Platelet
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University - Of The Common-
 ADDRESSEE: wealth System of Higher Education
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/893,929A
 FILING DATE: 19920605
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/803,630
 FILING DATE: December 3, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8383
 TELEFAX: (215) 568-5549
 TELEX: No. 5336667e
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 US-07-893-929A-4

Query Match 79.6%; Score 86; DB 1; Length 123;
 Best Local Similarity 76.5%; Pred. No. 3.6e-05;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 Db 1 DCPSDWSSYEGHCYRVF 17

RESULT 7

PCT-US92-10344-4
 Sequence 4, Application PC/TUS9210344
 GENERAL INFORMATION:

APPLICANT: Kirby, Edward P.
 APPLICANT: Peng, Man-ling
 TITLE OF INVENTION: Alboaggregins: Platelet
 TITLE OF INVENTION: Agonists Which Bind To Platelet
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Temple University - Of The Common-
 ADDRESSEE: wealth System of Higher Education
 STREET: 406 University Services Building
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: U.S.A.
 ZIP: 19122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: None
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US92-10344-4

Query Match 79.6%; Score 86; DB 5; Length 123;
Best Local Similarity 76.5%; Pred. No. 3.6e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYRVF 17

RESULT 8
US-07-614-443A-5
; Sequence 5, Application US/07614443A
; Patent No. 5342830
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/614,443A
; FILING DATE: 19901116
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22803-20003.00
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-614-443A-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 9
US-08-294-859-5
; Sequence 5, Application US/08294859
; Patent No. 5679542
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,859
; FILING DATE: 29-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-294-859-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSDWSSYEGHCYKVF 17

RESULT 10
US-08-481-676-5
; Sequence 5, Application US/08481676
; Patent No. 5744584
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,676
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/294,859
FILING DATE: 29-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2803-0003.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-481-676-5

Query Match 77.8%; Score 84; DB 1; Length 50;
Best Local Similarity 76.5%; Pred. No. 2.8e-05;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17
Db 1 DCPSDWSHGHGCHYKPF 17

RESULT 11
US-08-612-840A-1
Sequence 1, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Oblon

REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-840A-1

Query Match 76.9%; Score 83; DB 2; Length 38;
Best Local Similarity 70.6%; Pred. No. 2.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17
Db 3 ECPGWSYDRYKYPF 19

RESULT 12
US-08-612-840A-2
Sequence 2, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Oblon
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-840A-2

Query Match 76.9%; Score 83; DB 2; Length 126;
Best Local Similarity 70.6%; Pred. No. 9.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPGSSSYDRYCYKPF 19

RESULT 13
US-07-614-443A-1
; Sequence 1, Application US/07614443A
; Patent No. 5342830
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/614,443A
; FILING DATE: 19901116
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22803-20003.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-614-443A-1

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPGSSSYDRYCYKPF 19

RESULT 14
US-08-294-859-1
; Sequence 1, Application US/08294859
; Patent No. 5679542
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,859
; FILING DATE: 29-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-294-859-1

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||||
Db 3 ECPGSSSYDRYCYKPF 19

RESULT 15
US-08-481-676-1
; Sequence 1, Application US/08481676
; Patent No. 5744584
; GENERAL INFORMATION:
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: ANTITHROMBOSIS AGENTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,676
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/294,859
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2803-0003.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-481-676-1

Query Match 76.9%; Score 83; DB 1; Length 127;

Best Local Similarity 70.6%; Pred. No. 0.0001;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db :||| ||||: |||||
3 ECPSCWSSYDRYCYKPF 19

Search completed: December 8, 2003, 09:56:26
Job time : 4.69143 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:54:55 ; Search time 6.99429 Seconds
(without alignments)
452.044 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYRGFCVKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	108	100.0	17	11	US-09-938-114-4
2	83	76.9	149	10	US-09-969-763-3
3	81	75.0	29	11	US-09-938-114-3
4	81	75.0	110	10	US-09-969-763-10
5	81	75.0	129	11	US-09-938-114-2
6	78	72.2	151	10	US-09-929-230-2
7	78	72.2	151	12	US-10-226-420-2
8	74	68.5	126	10	US-09-969-763-1
9	71	65.7	152	10	US-09-929-230-5
10	71	65.7	152	12	US-10-226-420-5
11	66	61.1	144	10	US-09-929-230-8
12	66	61.1	144	12	US-10-226-420-8
13	61	56.5	1456	10	US-09-870-759-95
14	61	56.5	1456	12	US-09-751-708A-95
15	58	53.7	119	9	US-09-764-870-302
					Sequence 4, Appli
					Sequence 3, Appli
					Sequence 10, Appli
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 5, Appli
					Sequence 8, Appli
					Sequence 95, Appli
					Sequence 95, Appli
					Sequence 302, Appli

16 58 53.7 119 15 US-10-125-540-302 Sequence 302, App
17 58 53.7 293 10 US-09-978-295A-231 Sequence 231, App
18 58 53.7 293 10 US-09-978-697-231 Sequence 231, App
19 58 53.7 293 10 US-09-978-192A-231 Sequence 231, App
20 58 53.7 293 10 US-09-999-832A-231 Sequence 231, App
21 58 53.7 293 11 US-09-978-189-231 Sequence 231, App
22 58 53.7 293 11 US-09-978-608A-231 Sequence 231, App
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30 58 53.7 293 11 US-09-918-585A-231 Sequence 231, App
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35 58 53.7 293 11 US-09-978-187B-231 Sequence 231, App
36 58 53.7 293 11 US-09-978-643A-231 Sequence 231, App
37 58 53.7 293 12 US-09-978-375A-231 Sequence 231, App
38 58 53.7 293 12 US-09-978-188A-231 Sequence 231, App
39 58 53.7 293 12 US-09-978-298A-231 Sequence 231, App
40 58 53.7 293 12 US-10-137-870-422 Sequence 422, App
41 58 53.7 293 12 US-10-140-018-422 Sequence 422, App
42 58 53.7 293 12 US-10-140-021-422 Sequence 422, App
43 58 53.7 293 12 US-10-140-274-422 Sequence 422, App
44 58 53.7 293 12 US-10-140-471-422 Sequence 422, App
45 58 53.7 293 12 US-10-140-807-422 Sequence 422, App

ALIGNMENTS

RESULT 1

US-09-938-114-4
; Sequence 4, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-yu Xu, Dan Luo, Lian-Di Huang,
; Jin-Guo Ding, Fang Rong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-114-4
Query Match 100.0%; Score 108; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 2
US-09-969-763-3
; Sequence 3, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING THE SAME
; FILE REFERENCE: 214760U50
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Crotaalus harridus
US-09-969-763-3

Query Match 76.9%; Score 83; DB 10; Length 149;
Best Local Similarity 70.6%; Pred. No. 0.00024;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 26 ECPGSSSYDRYCYKPF 42

RESULT 3
US-09-938-114-3
; Sequence 3, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Rong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOTIC ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
```

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;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-938-114-3

Query Match 75.0%; Score 81; DB 11; Length 29;
Best Local Similarity 76.5%; Pred. No. 9.9e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCPSEWSSYEGFCYKPF 17

RESULT 4
US-09-969-763-10
; Sequence 10, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING THE SAME
; FILE REFERENCE: 214760U50
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 110
; TYPE: PRT
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; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-969-763-10

Query Match      75.0%; Score 81; DB 10; Length 110;
Best Local Similarity 70.6%; Pred. No. 0.00034;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 3 ECPGWSYRYCYKPF 19

RESULT 5
US-09-938-114-2
; Sequence 2, Application US/09938114
; Publication No. US20030022350A1
; GENERAL INFORMATION:
; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,
; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,
; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,
; Jin-Guo Ding, Fang Kong, Yan Liu and
; Hui-Ran Chen
; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE
; VENOM OF AGKISTRODON ACUTUS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,114
; FILING DATE: 23-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/058,740
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Chen, Anthony C.
; REGISTRATION NUMBER: 38,673
; REFERENCE/DOCKET NUMBER: 233/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-114-2

Query Match      75.0%; Score 81; DB 11; Length 129;
Best Local Similarity 76.5%; Pred. No. 0.0004;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 1 DCSWDSSYDQHCYKVF 17
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RESULT 6
US-09-929-230-2
; Sequence 2, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-2

Query Match      72.2%; Score 78; DB 10; Length 151;
Best Local Similarity 70.6%; Pred. No. 0.0012;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 20 DCPSDWSSYDQHCYKVF 36

RESULT 7
US-10-226-420-2
; Sequence 2, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-2

Query Match      72.2%; Score 78; DB 12; Length 151;
Best Local Similarity 70.6%; Pred. No. 0.0012;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 20 DCPSDWSSYDQHCYKVF 36

RESULT 8
US-09-969-763-1
; Sequence 1, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOYUKI
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHJI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
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; FILE REFERENCE: 214760USO
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Crotaallus horridus
US-09-969-763-1

Query Match 68.5%; Score 74; DB 10; Length 126;
Best Local Similarity 64.7%; Pred. No. 0.0038;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 3 ECPSGWSSYDQHCYRVF 19

RESULT 9

US-09-929-230-5
; Sequence 5, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-5

Query Match 65.7%; Score 71; DB 10; Length 152;
Best Local Similarity 64.7%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 24 DCPSGWSSYDQHCYRVF 40

RESULT 10

US-10-226-420-5
; Sequence 5, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-5

Query Match 65.7%; Score 71; DB 12; Length 152;
Best Local Similarity 64.7%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
Db 24 DCPSGWSSYDQHCYRVF 40

RESULT 11

US-09-929-230-8
; Sequence 8, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-09-929-230-8

Query Match 61.1%; Score 66; DB 10; Length 144;
Best Local Similarity 53.3%; Pred. No. 0.059;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
Db 12 DCPSDWYAYDQCYR 26

RESULT 12

US-10-226-420-8
; Sequence 8, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sistrurus miliarius
US-10-226-420-8

Query Match 61.1%; Score 66; DB 12; Length 144;
Best Local Similarity 53.3%; Pred. No. 0.059;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
Db 12 DCPSDWYAYDQCYR 26

RESULT 13

US-09-870-759-95
; Sequence 95, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30

Search completed: December 8, 2003, 10:07:06
Job time : 6.99429 secs

; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-95

Query Match 56.5%; Score 61; DB 10; Length 1456;
Best Local Similarity 64.3%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CPSEWSSYEGFCYK 15
|||:|:|:|:|
Db 362 CPSQWPFYAGHCYK 375

RESULT 14
US-09-751-708A-95
; Sequence 95, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 1456
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-751-708A-95

Query Match 56.5%; Score 61; DB 12; Length 1456;
Best Local Similarity 64.3%; Pred. No. 2.6;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CPSEWSSYEGFCYK 15
|||:|:|:|:|
Db 362 CPSQWPFYAGHCYK 375

RESULT 15
US-09-764-870-302
; Sequence 302, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 302
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-870-302

Query Match 53.7%; Score 58; DB 9; Length 119;
Best Local Similarity 61.5%; Pred. No. 0.68;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 CPSEWSSYEGFCY 14
||:|:|:|:|
Db 18 CPTSWLSFEGSCY 30

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 12:41:24 ; Search time 721.577 Seconds
(without alignments)
963.811 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	101	93.5	454	6	AR259041	Sequence
2	101	93.5	478	5	AY091756	Deinagkis
3	98	90.7	369	5	AY293866	Deinagkis
4	98	90.7	458	5	AF176421	Deinagkis
5	98	90.7	478	5	AY091761	Deinagkis
6	98	90.7	574	5	AF350324	Deinagkis
7	98	90.7	592	5	AB036881	Deinagkis
8	94	87.0	634	5	TFLFIXB	Trimeresuru
9	94	87.0	634	5	AF244901	Callosela
10	94	87.0	634	5	AF197915	Gloydus
11	93	86.1	688	5	AF540647	Deinagkis
12	86	79.6	664	5	AB019616	Agkistrod
13	84	77.8	583	5	AF125310	Gloydus
14	83	76.9	690	6	AR026653	Sequence
15	83	76.9	690	6	AX040807	Sequence
16	83	76.9	690	6	BD143687	Protein h
17	80	74.1	497	5	AY091758	Deinagkis
18	80	74.1	497	5	AB036880	Deinagkis
19	79	73.1	630	5	AF190827	Gloydus
20	78	72.2	375	5	AF387100	Deinagkis
21	78	72.2	483	6	AX427201	Sequence
22	78	72.2	483	5	AY091760	Deinagkis
23	77	71.3	733	5	AF176420	Deinagkis
24	76	70.4	678	5	TFLFIXA	Trimeresuru
25	76	70.4	683	5	AB046491	Trimeresuru
26	74	68.5	738	5	CDRNACVXB	Crotalus du
27	73	67.6	478	5	AY091755	Deinagkis
28	73	67.6	685	5	AF102902	Deinagkis
29	71	65.7	679	5	AB019615	Agkistrod
30	71	65.7	721	6	AX427204	Sequence
31	67	62.0	565	5	AY268948	Echis car
32	66	61.1	453	6	AX427203	Sequence
33	66	61.1	487	5	AF463521	Deinagkis
34	66	61.1	488	5	AY091754	Deinagkis
35	66	61.1	580	6	AX427207	Sequence
36	66	61.1	619	5	AF408448	Deinagkis
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38	64	59.3	170928	9	AL356740	Human DNA
39	62	57.4	4040	5	AF325324	Xenopus l
40	62	57.4	343050	1	AL935525	Lactobacil
41	61	56.5	448	9	HUMANR07	Human macro
42	61	56.5	495	5	AY091762	Deinagkis
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44	61	56.5	5185	9	HUMRA	Human manno
45	61	56.5	63525	9	AL928580	Human DNA

ALIGNMENTS

RESULT 1

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LOCUS AR259041 454 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 12 from patent US 6489451.
ACCESSION AR259041
VERSION AR259041.1 GI:27309526
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 454)
AUTHORS Li, B.X. and Cheng, X.
TITLE Antithrombin enzyme from the snake venom of agkistrodon acutus
JOURNAL Patent: US 6489451-A 12 03-DEC-2002;
FEATURES
Location/Qualifiers
1..454
/organism="unknown"
BASE COUNT 114 a 107 c 114 g 109 t 10 others
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Query Match: 93.52% Indels: 0
DB: 6 Gaps: 0
US-09-938-114-4 (1-17) x AR259041 (1-454)
Qy 1 AspCysProSerGluTrpSerSerTyGluGlyPheCysTyrlsProphe 17
Db 72 GATTGTCCTCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 122
RESULT 2
LOCUS AR091756 478 bp mRNA linear VRT 13-MAY-2002
DEFINITION Deinagkistrodon acutus clone 2100488 agkiscutacin B-chain mRNA, complete cds.
ACCESSION AR091756
VERSION AR091756.1 GI:20562934
KEYWORDS Deinagkistrodon acutus
SOURCE Deinagkistrodon acutus
ORGANISM Deinagkistrodon acutus
REFERENCE 1 (bases 1 to 478)
AUTHORS Yu, H., Xiang, K., Wang, Y. and Liu, J.
TITLE B chain of agkiscutacin from Deinagkistrodon acutus
JOURNAL Unpublished
AUTHORS Yu, H., Xiang, K., Wang, Y. and Liu, J.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular Biology, University of Science and Technology of China, School of Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
FEATURES
Location/Qualifiers
1..478
/organism="Deinagkistrodon acutus"
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BASE COUNT 126 a 109 c 126 g 117 t
ORIGIN

Alignment Scores:
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Score: 101.00 Matches: 16
Percent Similarity: 94.12% Conservative: 0
Best Local Similarity: 94.12% Mismatches: 1
Query Match: 93.52% Indels: 0
DB: 5 Gaps: 0
US-09-938-114-4 (1-17) x AY091756 (1-478)
Qy 1 AspCysProSerGluTrpSerSerTyGluGlyPheCysTyrlsProphe 17
Db 70 GATTGTCCTCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 120
RESULT 3
LOCUS AY293866 369 bp DNA linear VRT 09-JUN-2003
DEFINITION Deinagkistrodon acutus agkiscasin-b gene, partial cds.
ACCESSION AY293866
VERSION AY293866.1 GI:31559054
KEYWORDS Deinagkistrodon acutus
SOURCE Deinagkistrodon acutus
ORGANISM Deinagkistrodon acutus
REFERENCE 1 (bases 1 to 369)
AUTHORS Zha, X.D., Ren, B., Liu, J. and Xu, K.S.
TITLE Genomic DNA sequence of b chain of Agkiscasin, a C-type lectin-like protein from Agkistrodon acutus venom, and its evolutionary significance
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 369)
AUTHORS Zha, X.D., Ren, B., Liu, J. and Xu, K.S.
TITLE Direct Submission
JOURNAL Submitted (07-MAY-2003) Biology, School of Life Science, Anhui University, 3 Peixi Road, Hefei 230039, China
FEATURES
Location/Qualifiers
1..369
/organism="Deinagkistrodon acutus"
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1..369
/product="agkiscasin-b"
/note="C-type lectin-like protein"
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/product="agkiscasin-b"
/protein_id="AAP50528.1"
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BASE COUNT 107 a 83 c 88 g 91 t
ORIGIN
Alignment Scores:
Pred. No.: 2.78e-07 Length: 369
Score: 98.00 Matches: 15
Percent Similarity: 94.12% Conservative: 1
Best Local Similarity: 88.24% Mismatches: 1
Query Match: 90.74% Indels: 0
DB: 5 Gaps: 0
US-09-938-114-4 (1-17) x AY293866 (1-369)
Qy 1 AspCysProSerGluTrpSerSerTyGluGlyPheCysTyrlsProphe 17
Db 1 GATTGTCCTCTGAGTGCTCTCTATGAGGGCATTGCTACAGCCCTTC 51
RESULT 4
AF176421

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LOCUS      AF176421          458 bp      mRNA      linear      VRT 19-JAN-2000
DEFINITION Deinagkistrodon acutus agkiscutacin B chain mRNA, complete cds.
ACCESSION  AF176421
VERSION    AF176421.1 GI:6715114
KEYWORDS
SOURCE     Deinagkistrodon acutus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
            Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE  1 (bases 1 to 458)
AUTHORS    Cheng,X., Qian,X., Liu,Q., Li,B.X.Y., Ding,J., Xu,Z., Huang,W. and
            Liu,J.
TITLE      Agkiscutacin, a new fibrinolytic & anti-platelet protein from
            Agkistrodon acutus venom
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 458)
AUTHORS    Cheng,X., Liu,J., Li,B.X.Y. and Qian,Y.
TITLE      Direct Submission
JOURNAL    Submitted (08-AUG-1999) Dept. of Biochemistry and Molecular
            Biology, University of Science and Technology of China, School of
            Life-Science, Huangshan Road, Hefei, Anhui 230027, China
FEATURES   Location/Qualifiers
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                        /db_xref="taxon:36307"
                        /tissue_type="venom"
            CDS              3..443
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BASE COUNT 118 a 109 c 116 g 115 t
ORIGIN
Alignment Scores:
Pred. No.: 3.5e-07 Length: 458
Score: 98.00 Matches: 15
Percent Similarity: 94.12% Conservative: 1
Best Local Similarity: 88.24% Mismatches: 1
Query Match: 90.74% Indels: 0
DB: 5 Gaps: 0

US-09-938-114-4 (1-17) x AF176421 (1-458)

QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrrLysProPhe 17
Db 72 GATTGTCCTCTGATTGGTCTCTCTATGAAGGCGATTGCTACAGCCCTTC 122

RESULT 5
LOCUS      AY091761          478 bp      mRNA      linear      VRT 13-MAY-2002
DEFINITION Deinagkistrodon acutus clone 2101 AC1 1/2 B-chain mRNA, complete
            cds.
ACCESSION  AY091761
VERSION    AY091761.1 GI:20562942
KEYWORDS
SOURCE     Deinagkistrodon acutus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
            Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE  1 (bases 1 to 478)
AUTHORS    Yu,H., Xiang,K., Wang,Y. and Liu,J.
TITLE      B chain of AC1 1/2 from Deinagkistrodon acutus
JOURNAL    Unpublished

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REFERENCE  2 (bases 1 to 478)
AUTHORS    Yu,H., Xiang,K., Wang,Y. and Liu,J.
TITLE      Direct Submission
JOURNAL    Submitted (22-MAR-2002) Dept. of Biochemistry and Molecular
            Biology, University of Science and Technology of China, School of
            Life Science, Huangshan Road, Hefei, Anhui 230027, P.R. China
FEATURES   Location/Qualifiers
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BASE COUNT 127 a 107 c 125 g 119 t
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Alignment Scores:
Pred. No.: 3.66e-07 Length: 478
Score: 98.00 Matches: 15
Percent Similarity: 94.12% Conservative: 1
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Query Match: 90.74% Indels: 0
DB: 5 Gaps: 0

US-09-938-114-4 (1-17) x AY091761 (1-478)

QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyrrLysProPhe 17
Db 70 GATTGTCCTCTGATTGGTCTCTCTATGAAGGCGATTGCTACAGCCCTTC 120

RESULT 6
LOCUS      AF350324          574 bp      mRNA      linear      VRT 25-MAR-2001
DEFINITION Deinagkistrodon acutus agkiscasin-b mRNA, complete cds.
ACCESSION  AF350324
VERSION    AF350324.1 GI:13445903
KEYWORDS
SOURCE     Deinagkistrodon acutus
ORGANISM   Deinagkistrodon acutus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
            Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE  1 (bases 1 to 574)
AUTHORS    Zha,X. and Xu,K.
TITLE      Direct Submission
JOURNAL    Submitted (20-FEB-2001) Biochemical and Genetic Engineering Drugs,
            National Institute for Control of Pharmaceuticals and Biological
            Products, Tiantan Ximen, Xili Street 2, Beijing 10050, China
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BASE COUNT 170 a 134 c 133 g 137 t

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KEYWORDS
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ORGANISM Calloselasma rhodostoma (Malayan pit viper)
 Calloselasma rhodostoma
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 Viperidae; Crotalinae; Calloselasma.
REFERENCE
AUTHORS 1 (bases 1 to 438)
TITLE Chung, C.H., Au, L.C. and Huang, T.F.
 Molecular cloning and sequence analysis of aggretin, a
 collagen-like platelet aggregation inducer
JOURNAL Biochem. Biophys. Res. Commun. 263 (3), 723-727 (1999)
MEDLINE 99443731
PUBMED 10512747
REFERENCE 2 (bases 1 to 438)
AUTHORS Chung, C.H., Au, L.C. and Huang, T.F.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2000) Pharmacology, College of Medicine, National
 Taiwan University, No. 1, Sec. 1, Jen-Ai Rd., Taipei, Taiwan
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BASE COUNT 108 a 100 c 121 g 109 t
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 Best Local Similarity: 88.24% Mismatches: 2
 Query Match: 87.04% Indels: 0
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 US-09-938-114-4 (1-17) x AF244901 (1-438)
QY 1 AspCysProSerGluTrpSerTyrGluGlyPheCysTyrIlysProPhe 17
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Db 70 GATTGTCCTCTGGTGGTCTCTCTATGAAGGCATTGCTACAGCCCTTC 120
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RESULT 10
AF197915 634 bp mRNA linear VRT 01-NOV-2000
LOCUS Glyodius halys halysin B-chain precursor, mRNA, complete cds.
DEFINITION
ACCESSION AF197915
VERSION AF197915.1 GI:11066255
KEYWORDS
SOURCE Glyodius halys (halys viper)
ORGANISM Glyodius halys
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 Viperidae; Crotalinae; Glyodius.
REFERENCE
AUTHORS Koo, B.H., Sohn, Y.D., Kim, D.S., Jang, Y.S. and Chung, K.H.
TITLE A Novel Coagulation Factor Xa Inhibitor from Korean Snake
 (Agkistrodon halys) venom
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 634)
AUTHORS Sohn, Y.D., Koo, B.H., Kim, D.S., Jang, Y.S. and Chung, K.H.
TITLE Direct Submission

JOURNAL Submitted (22-OCT-1999) Cardiovascular center, Yonsei University
 College of Med., 134 Shinchon-dong, Seoul 120-752, Republic of
 Korea
FEATURES
source Location/Qualifiers
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RESULT 11
AF540647 688 bp mRNA linear VRT 26-SEP-2002
LOCUS Deinagkistrodon acutus agglutinin-beta 1 subunit precursor, mRNA,
 complete cds.
DEFINITION
ACCESSION AF540647
VERSION AF540647.1 GI:23321262
KEYWORDS
SOURCE Deinagkistrodon acutus
ORGANISM Deinagkistrodon acutus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 Viperidae; Crotalinae; Deinagkistrodon.
REFERENCE
AUTHORS Wang, W.J. and Huang, T.F.
TITLE A novel tetrameric venom protein, agglutinin from Agkistrodon
 acutus, acts as a glycoprotein Ib agonist
JOURNAL Thromb. Haemost. 86 (4), 1077-1086 (2001)
MEDLINE 21542539
PUBMED 11686327
REFERENCE 2 (bases 1 to 688)
AUTHORS Wang, W.-J., Ling, Q.-D. and Huang, T.-F.
TITLE Molecular structure and functional characterization of agglutinin,
 a tetrameric glycoprotein Ib-binding protein, from Formosan pit
 viper
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 688)
AUTHORS Wang, W.-J., Ling, Q.-D. and Huang, T.-F.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2002) Department of Nursing, Chang Gung Institute
 of Technology, 261, Wen-Hwa 1 Rd., Kwei-Shan, Tao-Yuan, Taiwan
 333-03, R.O.C.
FEATURES
source Location/Qualifiers
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 /organism="Deinagkistrodon acutus"

CDs

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DB:

US-09-938-114-4 (1-17) x AF540647 (1-688)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
Db 130 GATTGTCCTCTGAGTGGTCTCTCTATGAGGCGATTGCTACAGGCTTC 180

RESULT 12
LOCUS AB019616 664 bp mRNA linear VRT 14-NOV-1998
DEFINITION Agkistrodon blomhoffi mRNA for mamushigin beta, complete cds.
ACCESSION AB019616
VERSION AB019616.1 GI:3882118
KEYWORDS mamushigin beta.
SOURCE Agkistrodon blomhoffi
ORGANISM Agkistrodon blomhoffi
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
1 (sites)

REFERENCE
AUTHORS Sakurai, Y., Fujimura, Y., Kokubo, T., Imamura, K., Kawasaki, T.,
Handa, M., Suzuki, M., Matsui, T., Titani, K. and Yoshioka, A.
TITLE The cDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from
Agkistrodon halys blomhoffii venom
JOURNAL Thromb. Haemost. 79 (6), 1199-1207 (1998)
MEDLINE 98319530
PUBMED 9657448
REFERENCE 2 (bases 1 to 664)
AUTHORS Sakurai, Y. and Fujimura, Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1998) Yoshiniko Sakurai, Nara Medical University,
Department of Blood Transfusion Medicine, Shijo-cho 840, Kashihara,
Nara 634-8522, Japan (E-mail:ysakurai@nmu-gw.cc.naramed-u.ac.jp,
Tel:81-744-22-3051(ex.3288), Fax:81-744-29-0771)

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CDs

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US-09-938-114-4 (1-17) x AB019616 (1-664)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
Db 140 GATTGTCCTCTGATTGGTCTCTCTATGAGGCGATTGCTACAGGCTTC 190

RESULT 13

LOCUS AF125310 583 bp mRNA linear VRT 04-MAR-1999
DEFINITION Gloydius halys breviceaudus fibrinogen clotting inhibitor B chain
mRNA, complete cds.

ACCESSION AF125310
VERSION AF125310.1 GI:4337051

KEYWORDS

SOURCE

ORGANISM

Gloydius halys breviceaudus
Gloydius halys breviceaudus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.

1 (bases 1 to 583)

REFERENCE
AUTHORS Kim, D.S. and Koh, Y.S.
TITLE Purification and molecular cloning of snake venom fibrin clotting
inhibitor

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 583)

AUTHORS Kim, D.S. and Koh, Y.S.

TITLE Direct Submission
JOURNAL Submitted (01-FEB-1999) Biochemistry, Yonsei University, Seodaemun
ku Shinchon dong 134, Seoul 120-749, Korea

FEATURES

source

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BASE COUNT 151 a 137 c 150 g 145 t

ORIGIN

Alignment Scores:

Pred. No.: 0.000103 Length: 583

Score: 84.00 Matches: 14

Percent Similarity: 82.35% Conservative: 0

Best Local Similarity: 82.35% Mismatches: 3

Query Match: 77.78% Indels: 0

DB: 5 Gaps: 0

US-09-938-114-4 (1-17) x AF125310 (1-583)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17

Db 76 GATTGTCCTCTGTTGGTCTCTCTATGAGGCGATTGCTACAGCTCTTC 126

RESULT 14

AR026653
LOCUS AR026653 690 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5856126.
ACCESSION AR026653
VERSION AR026653.1 GI:5937493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 690)
AUTHORS Fukuchi,N., Yamamoto,H., Nagano,M., Kito,M., Tanaka,A., Ishii,K., Kobayashi,T. and Yoshimoto,R.
TITLE Peptide having anti-thrombus activity and method of producing the same
JOURNAL Patent: US 5856126-A 7 05-JAN-1999;
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Score: 83.00 Matches: 12
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Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
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US-09-938-114-4 (1-17) x AR026653 (1-690)

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Db 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191

RESULT 15

AX404807
LOCUS AX404807 690 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2 from Patent EP1195384.
ACCESSION AX404807
VERSION AX404807.1 GI:21438046
KEYWORDS
SOURCE Crotalus horridus horridus
ORGANISM Crotalus horridus horridus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalus.
REFERENCE 1
AUTHORS Fukuchi,N.P., Kito,M.P., Kayahara,T.P., Futaki,F.P., Ishikawa,K.C., Suzuki,E.C., Gondoh,K.C., Shima,N.C. and Yamada,N.C.
TITLE Snake proteins having antithrombotic activity
JOURNAL Patent: EP 1195384-A 2 10-APR-2002;
FEATURES
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CDS

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Alignment Scores:

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Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
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Query Match: 76.85% Indels: 0
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QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
Db 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191
Search completed: December 8, 2003, 16:08:47
Job time : 723.577 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 12:39:59 : Search time 58.3829 Seconds
(without alignments)
786.026 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	101	93.5	454	25	ABX93674	cDNA encoding Dein
2	94	87.0	633	22	AAI71877	Snake venom blood
3	84	77.8	583	24	AAI42016	Korean adder snake
4	83	76.9	690	16	AAQ89309	Snake venom anth
5	83	76.9	690	21	AAC81144	Snake venom anth
6	83	76.9	690	24	AAK99834	DNA encoding a sna
7	79	73.1	601	22	AAI71876	Snake venom blood
8	78	72.2	483	24	AAD32053	Pigmy rattlesnake
9	71	65.7	721	24	AAD32055	Pigmy rattlesnake
10	66	61.1	453	24	AAD32054	Pigmy rattlesnake
11	66	61.1	580	24	AAD32057	Pigmy rattlesnake
12	61	56.5	1062	23	AAS84910	DNA encoding novel
13	61	56.5	5140	13	AAQ24977	DNA encoding solub
14	61	56.5	5457	23	AAS84913	DNA encoding novel
15	60	55.6	432	24	AAD32058	Pigmy rattlesnake
16	58	53.7	618	22	AAS31223	Human cDNA encodin
17	58	53.7	618	23	AAS73634	DNA encoding novel
18	58	53.7	618	24	ABQ66547	Human polynucleoti
19	58	53.7	632	24	AAI42015	Korean adder snake
20	58	53.7	825	22	AAK86241	Human immune/haema
21	58	53.7	900	24	AB211972	Human polynucleoti
22	58	53.7	1017	24	AB211973	Human polynucleoti
23	58	53.7	1355	20	AA234085	Human polynucleoti
24	58	53.7	1355	21	AAC78506	Human PRO792 nucle
25	58	53.7	1355	21	AAC58240	Human PRO792 nucle
26	58	53.7	1355	21	AAI77635	Human PRO792 CDNA
27	58	53.7	1355	22	AAS21454	Human cDNA sequenc
28	58	53.7	1355	25	ACA03813	Human cDNA encodin
29	58	53.7	1355	25	ACQ04234	DNA encoding novel
30	58	53.7	1355	25	ABX89351	cDNA encoding huma
31	58	53.7	1355	25	ABX92457	Human immune/haema
32	58	53.7	1884	22	AAK86240	DNA encoding novel
33	57	52.8	621	24	ABK33326	Snake venom protei
34	57	52.8	716	17	AAI64829	Pigmy rattlesnake
35	57	52.8	725	24	AAD32059	Human bone marrow
36	56.5	52.3	5624	22	AAH89920	Pigmy rattlesnake
37	56	51.9	456	24	AAD32056	Pigmy rattlesnake
38	55	50.9	443	25	ABX41898	Bovine EST associa
39	55	50.9	781	22	AAL00590	Human reproductive
40	55	50.9	1067	24	ABK88776	DNA encoding huma
41	55	50.9	1482	24	AAD28152	Human secretion an
42	55	50.9	1585	22	AAL03775	Human reproductive
43	55	50.9	1585	22	AAL03776	Human reproductive
44	55	50.9	5085	25	AB224622	Mouse macrophage m
45	54	50.0	857	22	AAS31230	Human cDNA encodin

ALIGNMENTS

RESULT 1
ABX93674

ID ABX93674 standard; cDNA; 454 BP.

XX AC ABX93674;

XX DT 02-JUN-2003 (first entry)

XX DE cDNA encoding Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX KW Antithrombosis; ss; PCR; beta chain; fibrin hydrolysis; blood clot;
XX KW platelet aggregation; vaso-occlusive disorder; thromboembolic disorder;
XX KW myocardial infarction; restenosis; cancer; neurodegenerative disease;
XX KW angiopathic thrombosis; cerebral thrombosis; thromboangiitis obliterans;
XX KW ischaemic cerebral vascular disease; unstable angina; acute thrombosis;
XX KW unstable stenocardia; pulmonary embolism; deep vein thrombosis; oedema;
XX KW peripheral arterial occlusion; stroke; atherosclerosis; inflammation;

thrombosis.

XX OS Deinagkistrodon acutus.

XX FT Key Location/Qualifiers

XX FT CDS 3..443

XX FT /*tag= a

XX FT /product= "Antithrombosis enzyme beta chain"

XX FT /transl_except= (pos:216..218,aa:Xaa)

XX FT /transl_except= (pos:219..221,aa:Xaa)

XX FT /transl_except= (pos:222..224,aa:Xaa)

XX FT /transl_except= (pos:225..227,aa:Xaa)

XX FT /note= "Xaa = unknown"

XX FT 3..71

XX FT /*tag= b

XX FT /note= "Leader peptide"

XX FT 72..440

XX FT /*tag= c

XX FT /note= "Mature beta chain"

XX FT 217..226

XX FT /*tag= d

XX FT /note= "Unsequenced region could be 10-20 nucleotides in size"

XX FT

XX PN US6489451-B1.

XX XX

XX PD 03-DEC-2002.

XX XX

XX PF 10-APR-1998; 98US-0058740.

XX XX

XX PR 10-APR-1997; 97US-043886P.

XX XX

XX PA (HEFE-) HFEFI SIU FUNG USTC PHARM CO LTD.

XX PI Li BX, Cheng X;

XX PT WPI; 2003-352116/33.

XX DR P-PSDB; ABU08799.

XX XX

XX PT New purified Agkistrodon actus anti-thrombosis enzyme, useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, cerebral thrombosis and unstable angina

XX PS Disclosure; Fig 1; 19pp; English.

XX CC

XX CC The invention relates to a new Deinagkistrodon actus anti-thrombosis enzyme, where the enzyme hydrolyses fibrin, dissolves blood clots and prevents platelet aggregation. The anti-thrombosis enzyme was administered to rabbits intravenously. Thrombosis was determined before and after the administration at 0.5, 1.0, 2.0 and 3.0 hours by the Chandler method. The enzyme showed anti-thrombosis activity at 0.5 hour following administration at 0.005 micro/kg and this activity was increased significantly at 1.0 hour and at 0.01 micro /kg. The composition is useful for preventing and treating vaso-occlusive and thromboembolic disorders, including myocardial infarction, restenosis, angiotrophic thrombosis, cerebral thrombosis, ischaemic cerebral vascular diseases, unstable angina, acute thrombosis, unstable stenocardia, thromboangitis obliterans, pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion, stroke. It is also useful for treating atherosclerosis, oedema and inflammation, cancer and neurodegenerative diseases. The present sequence represents cDNA encoding the Deinagkistrodon acutus antithrombosis enzyme beta chain.

XX SQ Sequence 454 BP; 114 A; 107 C; 114 G; 109 T; 10 other;

Alignment Scores:

Pred. No.:	7,24e-07	Length:	454
Score:	101.00	Matches:	15
Percent Similarity:	94.12%	Conservative:	0
Best Local Similarity:	94.12%	Mismatches:	1
Query Match:	93.52%	Indels:	0
DB:	25	Gaps:	0

US-09-938-114-4 (1-17) x ABX93674 (1-454)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
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 Db 72 GATTGTCCTCTGAGTGGTCTCTCTATGAGGGGCGATTGCTACAAAGCCCTTC 122

RESULT 2

AAI71877

ID AAI71877 standard; DNA; 633 BP.

XX AC AAI71877;

XX DT 10-JAN-2002 (first entry)

XX DE Snake venom blood anticoagulant halyxin B chain coding sequence.

XX KW Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis; thrombosis; ds.

XX OS Agkistrodon halyx.

XX PN KR2001049671-A.

XX PD 15-JUN-2001.

XX PF 29-JUN-2000; 2000KR-0036591.

XX PR 29-JUN-1999; 99KR-0025105.

XX PA (BIOB-) BIOBUD CO LTD.

XX PI Jang YS, Jung GH, Kim DS, Koo BH, Son YD;

XX DR WPI; 2001-637330/73.

XX DR P-PSDB; AAMS1544.

XX PT Halyxin as blood anticoagulation protein separated from snake venom

XX PS Claim 1; Page 11; 21pp; Korean.

XX CC The invention relates to halyxin, a novel protein with very strong blood anticoagulation activity. The protein was separated from snake venom of Agkistrodon halyx brevicaudus (a Korean pit viper) and can be used in the treatment of thrombogenesis. The present sequence encodes the B chain of halyxin.

XX SQ Sequence 633 BP; 179 A; 142 C; 157 G; 155 T; 0 other;

Alignment Scores:

Pred. No.:	1,4e-05	Length:	633
Score:	94.00	Matches:	15
Percent Similarity:	88.24%	Conservative:	0
Best Local Similarity:	88.24%	Mismatches:	2
Query Match:	87.04%	Indels:	0
DB:	22	Gaps:	0

US-09-938-114-4 (1-17) x AAI71877 (1-633)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
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 Db 93 GATTGTCCTCTGAGTGGTCTCTCTATGAGGGGCGATTGCTACAAACCATTT 143

RESULT 3

AAI42016

ID AAI42016 standard; cDNA; 583 BP.

XX AC AAI42016;

XX DT 16-MAY-2002 (first entry)

XX DE Korean adder snake venom salmorin B chain protein cDNA sequence.

XX XX

KW Korean adder; ss; salmorin protein B chain; snake venom;
 KW fibrinogen clotting inhibition; thrombosis; prothrombin binding;
 KW thrombin binding; blood coagulation.

OS Agkistrodon halys brevicaudus.

XX Key Location/Qualifiers
 XX CDS 7..444
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 FT sig_peptide 7..75
 FT /*tag= b
 FT /note= "Signal peptide"
 FT mat_peptide 76..441
 FT /*tag= c
 FT /note= "Mature Salmorin B chain protein"
 FT 3'UTR 445..570
 FT /*tag= d
 FT polyA_signal 571..583
 FT /*tag= e

XX WO200214514-AL.

XX 21-FEB-2002.

XX 26-JUL-2001; 2001WO-KR01277.

XX 27-JUL-2000; 2000KR-0043470.

XX (BIOB-) BIOBUD CO LTD.

XX Chung K, Kim D, Koh Y;

XX WPI; 2002-241907/29.

XX P-PSDB; AAO14521.

XX New salmorin protein derived from venom of Korean adder Agkistrodon
 PT halys brevicaudus, useful for treating thrombosis by repressing
 PT fibrinogen clotting through repression of activation of prothrombin
 PT into thrombin

XX Claim 1; Fig 1B; 30pp; English.

XX The invention comprises the nucleotide and protein sequences of a
 CC salmorin protein derived from the venom of Korean adder. Salmorin protein
 CC is composed of an A chain and a B chain, and has inhibitory activity
 CC against fibrinogen clotting. The salmorin protein of the invention is
 CC useful for treating thrombosis, as it represses fibrinogen clotting
 CC potentially by binding to prothrombin and thrombin so as to delay blood
 CC coagulation. The present cDNA sequence encodes the Korean adder salmorin
 CC B chain protein.

XX SQ Sequence 583 BP; 151 A; 137 C; 150 G; 145 T; 0 other;

Alignment Scores:
 Pred. No.: 0.000487 Length: 583
 Score: 84.00 Matches: 14
 Percent Similarity: 82.35% Conservative: 0
 Best Local Similarity: 82.35% Mismatches: 3
 Query Match: 77.78% Indels: 0
 DB: 24 Gaps: 0

US-09-938-114-4 (1-17) x AAL42016 (1-583)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProphe 17
 Db 76 GAATGTCCTCGTGGTGGTCTCTATGAGGGCAATGCTACAGCTCTTC 126

RESULT 4

AAQ89309

ID AAQ89309 standard; cDNA; 690 BP.

XX AC AAQ89309;

XX 25-MAR-2003 (updated)
 DT 28-NOV-1995 (first entry)
 XX Snake venom antithrombotic oligopeptide cDNA.
 XX Antithrombotic peptide; snake venom; platelet binding inhibition;
 KW von Willebrand factors; Crotalus horridus horridus; ds.
 XX Crotalus horridus horridus.

XX Key Location/Qualifiers
 FT CDS 66..515
 FT /*tag= a

XX WO9508573-AL.

XX 30-MAR-1995.

XX 21-SEP-1994; 94WO-JP01555.

XX 22-SEP-1993; 93JP-0236975.

XX (AJIN) AJINOMOTO KK.

XX Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;

XX Tanaka A, Yamamoto H, Yoshimoto R;

XX WPI; 1995-139559/18.

XX P-PSDB; AAR71981.

XX Single-chain antithrombotic peptide - obtained by cleaving an
 PT oligopeptide from snake venom to break inter-chain di:sulphide
 PT bonds but preserve intra-chain di:sulphide bonds

XX Example 2; Pages 47-48; 84pp; Japanese.

XX AAR71978 and AAR71979 are snake venom derived antithrombotic peptides,
 CC specifically from the snake venom oligopeptide AAR71981, encoded by
 CC AAQ89309. These peptides have the advantage of avoiding significant
 CC thrombocytopenia when administered at the minimum dose, for in vivo
 CC inhibition of platelet von Willebrand factor binding.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;

Alignment Scores:
 Pred. No.: 0.00086 Length: 690
 Score: 83.00 Matches: 12
 Percent Similarity: 88.24% Conservative: 3
 Best Local Similarity: 70.59% Mismatches: 2
 Query Match: 76.85% Indels: 0
 DB: 16 Gaps: 0

US-09-938-114-4 (1-17) x AAQ89309 (1-690)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIysProphe 17
 Db 141 GAATGTCCTCGGTTGGTCTCTCTATGATCGGTATGCTACAGCCCTTC 191

RESULT 5

AAC61144

ID AAC61144 standard; DNA; 690 BP.

XX AC AAC61144;

XX 07-FEB-2001 (first entry)

XX DNA encoding a snake venom derived protein.

XX Subunit peptide production; snake venom; rattlesnake; thrombolytic;
 KW von Willebrand's factor; blood platelet-inhibitory activity; ds.

OS Crotalus horridus horridus.
XX WO200059926-A1.
XX 12-OCT-2000.
XX 31-MAR-2000; 2000WO-JP02127.
XX 02-APR-1999; 99JP-0096073.
XX (AJIN) AJINOMOTO CO INC.
XX Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;
XX WPI; 2000-664985/64.
XX P-PSDB; AAY85628.
XX Producing physiologically-active subunit peptides originating in
XX polymer proteins by denaturation and specific separation, with lower
XX antigenicity but improved solubility and stability, e.g. blood
XX platelet-binding inhibitors -
XX Disclosure; Page 46; 51pp; Japanese.
XX This invention relates to a method for the production of a subunit
XX peptide originating from a polymer protein with disulphide bonds within
XX and between subunits. The method comprises denaturing the protein or its
XX subunit using a protein denaturing agent in a solution, removing the
XX agent in the presence of a polyoxyalkyl polyether which reacts with a
XX thiol group and unwinds the subunit, and separating the polyoxyalkyl
XX polyether-bound subunit peptide. The method can be used for producing
XX physiologically-active subunit peptides for polymer proteins e.g. snake
XX venom-originated dimer peptide with blood platelet-inhibitory activity
XX on von Willebrand's factor. The peptides produced have platelet-binding
XX inhibitory, and thrombolytic activity. The present sequence represents
XX DNA encoding rattlesnake protein used in an example illustrating the
XX method of the invention.
XX Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
SQ Alignment Scores:
Pred. No.: 0.00086 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 21 Gaps: 0
US-09-938-114-4 (1-17) x AAC61144 (1-690)
QY 1 AspCysProSerGluTyrSerSerTyrGluGlyPheCysTyrLysProphe 17
DB 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATGCTACAGCCCTTC 191
RESULT 6
AAK99834
ID AAK99834 standard; DNA; 690 BP.
XX AC AAK99834;
XX 19-JUL-2002 (first entry)
XX DE DNA encoding the antithrombotic wild-type rattlesnake protein.
XX Thrombolytic; glycoprotein Ib-binding protein; snake venom; rattlesnake;
XX antithrombotic; glycoprotein Ib; long half life; low antigenicity;
XX drug efficacy; gene; ds.
XX Crotalus horridus horridus.
XX Key Location/Qualifiers
FH 66..515
FT CDS /*tag= a
FT

/product= "Antithrombotic wild-type rattlesnake protein"
FT EPI195384-A1.
XX 10-APR-2002.
XX 04-OCT-2001; 2001EP-0123277.
XX 04-OCT-2000; 2000JP-0305279.
XX (AJIN) AJINOMOTO CO INC.
XX Fukuchi N, Kito M, Kayahara T, Futaki F, Ishikawa K, Suzuki E;
XX Gondeh K, Shimba N, Yamada N;
XX WPI; 2002-364482/40.
XX P-ESDB; AAO20974.
XX Glycoprotein Ib-binding protein, useful for treating thrombosis,
XX comprises specific mutations in protein originating from snake venom -
XX Example 1; Page 25; 49pp; English.
XX The invention relates to a glycoprotein Ib-binding protein, originating
XX from snake venom, comprising specific mutations and antithrombotic
XX activity. Glycoprotein Ib-binding protein is used in a drug having
XX antithrombotic activity. Glycoprotein Ib-binding protein has a high
XX binding activity to glycoprotein Ib, a long half life/drug efficacy
XX retention in blood, and low antigenicity. This polynucleotide sequence
XX represents DNA of the wild-type rattlesnake protein of the invention.
XX Sequence 690 BP; 167 A; 180 C; 170 G; 173 T; 0 other;
SQ Alignment Scores:
Pred. No.: 0.00086 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 24 Gaps: 0
US-09-938-114-4 (1-17) x AAK99834 (1-690)
QY 1 AspCysProSerGluTyrSerSerTyrGluGlyPheCysTyrLysProphe 17
DB 141 GAATGTCCTCCGGTTGGTCTCTCTATGATCGGTATGCTACAGCCCTTC 191
RESULT 7
AAI71876
ID AAI71876 standard; DNA; 601 BP.
XX AC AAI71876;
XX 10-JAN-2002 (first entry)
XX DE Snake venom blood anticoagulant halyxin A chain coding sequence.
XX Snake; pit viper; venom; halyxin; anticoagulant; thrombogenesis;
XX thrombosis; ds.
XX Agkistrodon halys.
XX KR2001049671-A.
XX 15-JUN-2001.
XX 29-JUN-2000; 2000KR-0036591.
XX 29-JUN-1999; 99KR-0025105.
XX (BIOB-) BIOBUD CO LTD.
XX Jang YS, Jung GH, Kim DS, Koo BH, Son YD;
PI


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XX WPI; 2001-637330/73.
DR P-PSDB; AAM51543.
XX
XX Halyxin as blood anticoagulation protein separated from snake venom -
XX Claim 1; Page 9; 21pp; Korean.
XX
XX The invention relates to halyxin, a novel protein with very strong
XX blood anticoagulation activity. The protein was separated from snake
XX venom of Agkistrodon haly brevicaudus (a Korean pit viper) and can
XX be used in the treatment of thrombogenesis. The present sequence
XX encodes the A chain of halyxin.
XX
SQ Sequence 601 BP; 166 A; 133 C; 163 G; 139 T; 0 other;

Alignment Scores:
Pred. No.: 0.00313 Length: 601
Score: 79.00 Matches: 13
Percent Similarity: 76.47% Conservative: 0
Best Local Similarity: 76.47% Mismatches: 4
Query Match: 73.15% Indels: 0
DB: 22 Gaps: 0

US-09-938-114-4 (1-17) x AAI71876 (1-601)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 93 GATTGTCCCTCGTGGTGGCTCTCTATGAGGGCATTGCTACACATCTTC 143

RESULT 8
AAD32053
ID AAD32053 standard; DNA; 483 BP.
AC AAD32053;
XX
XX 18-JUN-2002 (first entry)
XX
XX Pigmy rattlesnake venom gland protein, Zsnk2 gene.
XX
XX Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
XX platelet aggregation; gene; Zsnk2; ds.
XX
XX Sistrurus miliarius.
XX
XX Key Location/Qualifiers
XX CDS 3..458
XX /*tag= a
XX /product= "Zsnk2 protein"
XX /note= "CDS does not include start codon"
XX /partial
XX sig_peptide 3..59
XX /*tag= b
XX mat_peptide 60..455
XX /*tag= c
XX /product= "Mature Zsnk2 protein"
XX
XX WO200214364-A2.
XX
XX 21-FEB-2002.
XX
XX 13-AUG-2001; 2001WO-US25310.
XX
XX 14-AUG-2000; 2000US-225072P.
XX 14-AUG-2000; 2000US-225087P.
XX 15-AUG-2000; 2000US-225489P.
XX 15-AUG-2000; 2000US-225490P.
XX 20-DEC-2000; 2000US-356997P.
XX
XX (Zymo ) ZYMOGENETICS INC.
XX
XX Sheppard PO, Bishop PD;
XX
XX
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DR WPI; 2002-269180/31.
DR P-PSDB; AAE20178.
XX
XX New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
XX affect blood coagulation and platelet aggregation system, useful in
XX therapy and diagnostics, or as tools in the study of genetics or
XX molecular biology -
XX
XX Claim 5; Page 71-72; 79pp; English.
XX
XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
XX venom gland proteins, which affect blood coagulation and platelet
XX aggregation system. The polypeptides, which affect blood coagulation and
XX platelet aggregation system, are useful in therapy and diagnostics. The
XX polypeptides are also useful as an educational tool in laboratory
XX practical kits for courses related to genetics and molecular biology,
XX protein chemistry and antibody production and analysis. The
XX polynucleotide or polypeptide can be used as standards or as unknowns
XX for testing purposes. The polypeptides are also useful in identifying
XX proteins by western blotting, protein purification, determining the
XX weight of expressed polypeptides as a ratio to total protein expressed,
XX identifying peptide cleavage sites, coupling amino and carboxyl terminal
XX tags, mass spectrometry, circular dichroism to determine conformation or
XX affinity chromatography columns to purify the protein, cloning or
XX sequencing. The present sequence is Sistrurus miliarius venom gland
XX protein, Zsnk2 gene.
XX
XX Sequence 483 BP; 129 A; 112 C; 123 G; 119 T; 0 other;

Alignment Scores:
Pred. No.: 0.00346 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservative: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 24 Gaps: 0

US-09-938-114-4 (1-17) x AAD32053 (1-483)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 60 GATTGTCCCTCTGACCTGGTCTCTATGATCAGCATTTGCTACAGGTCTTC 110

RESULT 9
AAD32055
ID AAD32055 standard; DNA; 721 BP.
AC AAD32055;
XX
XX 18-JUN-2002 (first entry)
XX
XX Pigmy rattlesnake venom gland protein, Zsnk3 gene.
XX
XX Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
XX platelet aggregation; gene; Zsnk3; ds.
XX
XX Sistrurus miliarius.
XX
XX Key Location/Qualifiers
XX CDS 91..549
XX /*tag= a
XX /product= "Zsnk3 protein"
XX /91..159
XX sig_peptide /*tag= b
XX mat_peptide 160..546
XX /*tag= c
XX /product= "Mature Zsnk3 protein"
XX
XX WO200214364-A2.
XX
XX 21-FEB-2002.
XX
XX 13-AUG-2001; 2001WO-US25310.
XX
XX
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XX 14-AUG-2000; 2000US-225072P.
 PR 14-AUG-2000; 2000US-225087P.
 PR 15-AUG-2000; 2000US-225489P.
 PR 15-AUG-2000; 2000US-225490P.
 PR 20-DEC-2000; 2000US-356997P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Bishop PD;
 PI WPI; 2002-269180/31.
 DR P-PSDB; AAE20179.
 XX New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 PT affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology -
 XX Claim 5; Page 73-74; 79pp; English.
 XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein, Zsnk3 gene.
 XX Sequence 721 BP; 192 A; 167 C; 203 G; 159 T; 0 other;
 SQ Alignment Scores:
 Pred. No.: 0.0725 Length: 721
 Score: 71.00 Matches: 11
 Percent Similarity: 76.47% Conservative: 2
 Best Local Similarity: 64.71% Mismatches: 4
 Query Match: 65.74% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32055 (1-721)
 QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
 Db 160 GATTGCCCTCTGGTGGTCTCTATGATCAGCATGTCACAGGCTTC 210
 RESULT 10
 AAD32054
 ID AAD32054 standard; DNA; 453 BP.
 XX AAD32054;
 AC AAD32054;
 XX 18-JUN-2002 (first entry)
 DT Pigmy rattlesnake venom gland protein Zsnk2, degenerate nucleic acid.
 DE Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 XX platelet aggregation; ds.
 KW Sistrurus miliarius.
 XX WO200214364-A2.
 PN 21-FEB-2002.
 XX

PF 13-AUG-2001; 2001WO-US25310.
 XX 14-AUG-2000; 2000US-225072P.
 PR 14-AUG-2000; 2000US-225087P.
 PR 15-AUG-2000; 2000US-225489P.
 PR 15-AUG-2000; 2000US-225490P.
 PR 20-DEC-2000; 2000US-356997P.
 XX (ZYMO) ZYMOGENETICS INC.
 XX Sheppard PO, Bishop PD;
 PI WPI; 2002-269180/31.
 DR New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 XX affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology -
 XX Disclosure; Page 72-73; 79pp; English.
 XX The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein Zsnk2, degenerate nucleic acid.
 XX Sequence 453 BP; 74 A; 32 C; 84 G; 70 T; 193 other;
 SQ Alignment Scores:
 Pred. No.: 0.256 Length: 453
 Score: 66.00 Matches: 9
 Percent Similarity: 64.71% Conservative: 2
 Best Local Similarity: 52.94% Mismatches: 6
 Query Match: 61.11% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32054 (1-453)
 QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
 Db 58 GAYTGYCCNWSNGAYTGGWSNNTAYGAYCARCAVYGTAYAAAGTNTTY 108
 RESULT 11
 AAD32057
 ID AAD32057 standard; DNA; 580 BP.
 XX AAD32057;
 AC AAD32057;
 XX 18-JUN-2002 (first entry)
 DT Pigmy rattlesnake venom gland protein, Zsnk4 gene.
 DE Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 XX platelet aggregation; gene; Zsnk4; ds.
 KW Sistrurus miliarius.
 XX OS
 XX Key Location/Qualifiers
 PH CDS 3..437
 FT /*tag= a
 FT /product= "Zsnk4 protein"


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XX AC AAQ24977;
XX DT 25-MAR-2003 (updated)
XX DT 18-NOV-1992 (first entry)
XX DE DNA encoding soluble mannose receptor peptide.
XX DE
XX KW Soluble mannose receptor peptide; ss DNA; receptor binding;
XX KW cancer cells; targeting; probe; DNA delivery; cell marker;
XX KW fusion molecule; AZT; ricin; pertussis; cholera toxin; liposome;
XX KW therapeutic agent; diagnostic agent; opportunistic infections;
XX KW immunocompromised patients; HIV.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 59..4429
XX FT /*tag= a
XX FN WO9207579-A1.
XX PD 14-MAY-1992.
XX PF 06-NOV-1991; 91WO-US08320.
XX PR 06-NOV-1990; 90US-0609915.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Ezekowitz RAB;
XX DR WPI; 1992-183410/22.
XX DR P-PSDB; AAR24033.
XX PT Soluble extracellular recombinant mannose receptor protein
XX PT fragments - target mannose expressing cells for treatment and
XX PT diagnosis of infections, cancer, etc.
XX PS Disclosure; page 21-27; 37pp; English.
XX CC The mannose receptor protein (MRP), or at least one carbohydrate
XX CC recognition domain of it derived from an extracellular portion, can
XX CC specifically bind pro- or eukaryotic pathogens, eg bacteria, fungi
XX CC or viruses, with exposed configurations of mannose,
XX CC N-acetylglucosamine or fucose on their cell wall or on the envelope
XX CC glycoprotein. The protein lacks the MRP transmembrane and cytoplasmic
XX CC regions and is capable of specifically targeting cells expressing the
XX CC specified proteins. The MRPs can also target cancer cells which have
XX CC any exposed mannose residues resulting from aberrant glycosylation.
XX CC The proteins can be used as probes for such cells, or as fusion
XX CC molecules for delivery of specific molecules, eg AZT, ricin, pertussis
XX CC or cholera toxins, or CD4 to fix complement, or as an in vivo marker
XX CC for immune system cells. The hybrid molecules are esp. capable of
XX CC causing an effector molecule to be targeted to a cell, eg a virus.
XX CC MRP and antibodies raised to it are also useful as therapeutic or
XX CC diagnostic agents, eg for Leishmania protozoan parasites, Pneumocystis
XX CC carinii, Candida albicans, Microbacterium tuberculosis, HIV or
XX CC influenza virus. The antibodies are also useful to purify the MRP.
XX CC The protein may be administered as a coating on a liposome, or as a
XX CC powder or lotion.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 5140 BP; 1598 A; 994 C; 1175 G; 1373 T; 0 other;

Alignment Scores:
Pred. No.: 30.3 Length: 5140
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 56.48% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x AAQ24977 (1-5140)
QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 1142 TGTCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACCAAG 1183

RESULT 14
AAS84913
ID AAS84913 standard; cDNA; 5457 BP.
XX AC AAS84913;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #20717.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR P-PSDB; ABG20726.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
XX PS Claim 1; SEQ ID No 20717; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 5457 BP; 1645 A; 1081 C; 1276 G; 1455 T; 0 other;

Alignment Scores:
Pred. No.: 32.5 Length: 5457
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4

```

Query Match: 56.48% Indels: 0
 DB: 23 Gaps: 0
 US-09-938-114-4 (1-17) x AAS84913 (1-5457)
 Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
 Db 1401 TGTCTAGTCAGTGGTGGCCGTATGCCGTGCTACTGTACAAAG 1442

RESULT 15

AAD32058
 ID AAD32058 standard; DNA; 432 BP.
 XX
 AC AAD32058;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Pigmy rattlesnake venom gland protein Zsnk4, degenerate nucleic acid.
 XX
 KW Pigmy rattlesnake; venom gland protein; blood coagulation; therapy;
 KW platelet aggregation; ds.
 XX
 OS Sistrurus miliarius.

XX
 FN WO200214364-A2.

XX
 PD 21-FEB-2002.

XX
 PF 13-AUG-2001; 2001WO-US25310.

XX
 PR 14-AUG-2000; 2000US-225072P.

PR 14-AUG-2000; 2000US-225087P.

PR 15-AUG-2000; 2000US-225489P.

PR 15-AUG-2000; 2000US-225490P.

PR 20-DEC-2000; 2000US-356997P.

XX
 PA (ZYMO) ZYMOGENETICS INC.

XX
 PI Sheppard PO, Bishop PD;

XX
 WPI; 2002-269180/31.

XX
 PT New pigmy rattlesnake (Sistrurus miliarius) venom gland proteins, which
 PT affect blood coagulation and platelet aggregation system, useful in
 PT therapy and diagnostics, or as tools in the study of genetics or
 PT molecular biology

XX
 PS Disclosure; Page 76; 79pp; English.

XX
 CC The invention relates to new pigmy rattlesnake (Sistrurus miliarius)
 CC venom gland proteins, which affect blood coagulation and platelet
 CC aggregation system. The polypeptides, which affect blood coagulation and platelet
 CC platelet aggregation system, are useful in therapy and diagnostics. The
 CC polypeptides are also useful as an educational tool in laboratory
 CC practical kits for courses related to genetics and molecular biology,
 CC protein chemistry and antibody production and analysis. The
 CC polynucleotide or polypeptide can be used as standards or as unknowns
 CC for testing purposes. The polypeptides are also useful in identifying
 CC proteins by western blotting, protein purification, determining the
 CC weight of expressed polypeptides as a ratio to total protein expressed,
 CC identifying peptide cleavage sites, coupling amino and carboxyl terminal
 CC tags, mass spectrometry, circular dichroism to determine conformation or
 CC affinity chromatography columns to purify the protein, cloning or
 CC sequencing. The present sequence is Sistrurus miliarius venom gland
 CC protein Zsnk4, degenerate nucleic acid.

XX
 SQ Sequence 432 BP; 91 A; 34 C; 84 G; 55 T; 168 other;

Alignment Scores:

Align. No.: 2.16 Length: 432
 Score: 60.00 Matches: 7
 Percent Similarity: 78.57% Conservative: 4
 Best Local Similarity: 50.00% Mismatches: 3

Query Match: 55.56% Indels: 0
 DB: 24 Gaps: 0
 US-09-938-114-4 (1-17) x AAD32058 (1-432)
 Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
 Db 34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGTAY 75

Search completed: December 8, 2003, 14:04:49
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:49:04 ; Search time 13.4057 Seconds
(without alignments)
559.725 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCFSEWSSYEGFCVKPF 17

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame.p2n.model -DRV=xlh

-Q/cgn2_1/USPTO.spool/US0938114/runat_08122003_091001_22878/app_query.fasta_1.725

-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=ptlo -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000

-USER=US0938114 @C9N 1 1 95 -runat_08122003_091001_22878 -NCFU=6 -ICPU=3

-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DRV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101	93.5	454	4	US-09-058-740-12
2	83	76.9	690	2	Sequence 12, Appl
3	54	50.0	1600	4	Sequence 7, Appl
4	52	48.1	360	3	Sequence 1, Appl
5	52	48.1	405	3	Sequence 4, Appl
6	52	48.1	405	3	Sequence 3, Appl
7	52	48.1	645	3	Sequence 7, Appl
8	52	48.1	693	3	Sequence 12, Appl
9	52	48.1	699	3	Sequence 13, Appl
10	52	48.1	1212	3	Sequence 11, Appl
11	52	48.1	1212	3	Sequence 9, Appl
12	52	48.1	1212	3	Sequence 10, Appl
					Sequence 11, Appl

13	48.1	1222	3	US-08-543-246B-5	Sequence 5, Appl
14	48.1	1223	4	US-09-016-434-1347	Sequence 1347, Ap
15	48.1	1312	4	US-09-517-605-1	Sequence 1, Appl
16	48.1	1333	3	US-08-543-246B-15	Sequence 15, Appl
17	48.1	1387	3	US-08-543-246B-1	Sequence 1, Appl
18	48.1	1643	4	US-09-517-605-16	Sequence 16, Appl
19	47.2	1764	2	US-08-504-459-3	Sequence 3, Appl
20	51	3259	5	PCT-US95-03747-1	Sequence 1, Appl
21	50	46.3	216	4	Sequence 583, App
22	50	46.3	5169	4	Sequence 2, Appl
23	50	46.3	11225	6	Patent No. 5182210
24	49	45.4	1422	3	Sequence 25, Appl
25	49	45.4	1422	5	Sequence 30, Appl
26	49	45.4	2076	4	Sequence 51, Appl
27	49	45.4	9401	2	Sequence 1, Appl
28	49	45.4	9416	3	Sequence 19, Appl
29	49	45.4	9416	4	Sequence 19, Appl
30	49	45.4	124884	4	Sequence 76, Appl
31	48	44.4	402	3	Sequence 10, Appl
32	48	44.4	558	2	Sequence 5, Appl
33	48	44.4	648	3	Sequence 14, Appl
34	48	44.4	1755	3	Sequence 8, Appl
35	48	44.4	1806	4	Sequence 1534, Ap
36	48	44.4	2376	2	Sequence 4, Appl
37	48	44.4	3843	4	Sequence 1430, Ap
38	48	44.4	5337	4	Sequence 1588, Ap
39	47	43.5	152	3	Sequence 40, Appl
40	47	43.5	393	3	Sequence 22, Appl
41	47	43.5	501	3	Sequence 20, Appl
42	47	43.5	600	5	Sequence 3, Appl
43	47	43.5	1104	3	Sequence 1, Appl
44	47	43.5	1227	3	Sequence 3, Appl
45	47	43.5	2045	3	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-09-058-740-12

; Sequence 12, Application US/09058740

; Patent No. 6489451

; GENERAL INFORMATION:

; APPLICANT: Chun Wang, Benjamin XY Li, Xin Cheng,

; Jing Liu, Li-Wen Niu, Wan-Zhi Huang,

; Zhen-Yu Xu, Dan Luo, Lian-Di Kang,

; Jin-Guo Ding, Fang Rong, Yan Liu and

; Hui-Ran Chen

; TITLE OF INVENTION: AN ANTITHROMBOSIS ENZYME FROM THE SNAKE

; CORRESPONDENCE ADDRESS: VENOM OF AGKISTRODON ACUTUS

; NUMBER OF SEQUENCES: 12

; ADDRESS: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/058,740

; FILING DATE: 10-Apr-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Chen, Anthony C.

REGISTRATION NUMBER: 38,673
REFERENCE/DOCKET NUMBER: 233/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 3...440
OTHER INFORMATION: "N" stands for any base.
"Xaa" stands for any amino acid.
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-058-740-12
Alignment Scores:
Pred. No.: 3.26e-08 Length: 454
Score: 101.00 Matches: 16
Percent Similarity: 94.12% Conservative: 0
Best Local Similarity: 94.12% Mismatches: 1
Query Match: 93.52% Indels: 0
DB: 4 Gaps: 0
US-09-938-114-4 (1-17) x US-09-058-740-12 (1-454)
QY 1 AspCysProSerGluTrpSerSerTyrgluGlyPheCysTyrIysProPhe 17
Db 72 GAATGTCCTCTGAGTGGTCTCTCTATGAGGGCATTGCTACAGCCCTTC 122
RESULT 2
US-08-612-840A-7
Sequence 7, Application US/08612840A
Patent No. 5856126
GENERAL INFORMATION:
APPLICANT: FUKUCHI, Naoyuki
APPLICANT: YAMAMOTO, Hiroshi
APPLICANT: NAGANO, Mitsuyo
APPLICANT: KITO, Morikazu
APPLICANT: TANAKA, Akiko
APPLICANT: ISHII, Koichi
APPLICANT: KOBAYASHI, Tsuyoshi
APPLICANT: YOSHIMOTO, Ryota
TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND
TITLE OF INVENTION: METHOD OF PRODUCING THE SAME
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Obion, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,840A
FILING DATE: 20-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-236975
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5856126man F. Obion
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Crotaus horridus horridus
STRAIN:
FEATURE:
NAME/KEY: CDS
LOCATION: 56..512
US-08-612-840A-7
Alignment Scores:
Pred. No.: 5.53e-05 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 2 Gaps: 0
US-09-938-114-4 (1-17) x US-08-612-840A-7 (1-690)
QY 1 AspCysProSerGluTrpSerSerTyrgluGlyPheCysTyrIysProPhe 17
Db 141 GAATGTCCTCGTGGTCTCTCTATGATCGGTATTGCTACAGCCCTTC 191
RESULT 3
US-09-585-228-1
Sequence 1, Application US/09585228
Patent No. 6531576
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: West, James W.
APPLICANT: HOLLY, Richard D.
APPLICANT: Burkhead, Steven K.
TITLE OF INVENTION: FOUR-HELICAL BUNDLE PROTEIN ZSIG81
FILE REFERENCE: 99-13
CURRENT APPLICATION NUMBER: US/09/585,228
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: US 60/137,057
EARLIER FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1600
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (134)...(655)
NAME/KEY: sig_peptide
LOCATION: (134)...(184)
US-09-585-228-1
Alignment Scores:
Pred. No.: 10.9 Length: 1600
Score: 54.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0
US-09-938-114-4 (1-17) x US-09-585-228-1 (1-1600)
QY 2 CysProSerGluTrpSerSerTyrgluGlyPheCysTyr 14
|||||

Db 1420 TGCCCCAGCTCTGGCACCATTATTCGTCTGCTTT 1458

RESULT 4
US-08-543-246B-4
; Sequence 4, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-4

Alignment Scores:
Pred. No.: 3 61 Length: 360
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-4 (1-360)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
||||| :|||
Db 16 TGTCTGAGAGTGGATTACATATTCACACAGTTGTAC 54
||||| :|||

RESULT 5
US-08-543-246B-3
; Sequence 3, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation

; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-543-246B-3

Alignment Scores:
Pred. No.: 4 18 Length: 405
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-3 (1-405)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
||||| :|||
Db 61 TGTCTGAGAGTGGATTACATATTCACACAGTTGTAC 99
||||| :|||

RESULT 6
US-08-543-246B-7
; Sequence 7, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation

STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-7

Alignment Scores:
Pred. No.: 4.18 Length: 405
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-7 (1-405)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 61 TGTCTGAGAGTGGATTACATATTCACAGTTGTAT 99

RESULT 7
US-08-543-246B-12
Sequence 12, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for
TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glyn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-12

Alignment Scores:
Pred. No.: 7.5 Length: 645
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-12 (1-645)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 301 TGTCTGAGAGTGGATTACATATTCACAGTTGTAT 339

RESULT 8
US-08-543-246B-13
Sequence 13, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DNA and amino acid sequence specific for
TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glyn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA: PCT/US92/02469
APPLICATION NUMBER: 26,389
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA: PCT/US92/02469
APPLICATION NUMBER: US 08/122,514
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-13

Alignment Scores:
Pred. No.: 8.2 Length: 693
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-13 (1-693)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 349 TGTCCTGAGAGTGGATTACATATCCACAGTTGTAT 387

RESULT 9

US-08-543-246B-11
Sequence 11, Application US/08543246B
Patent No. 6262244
GENERAL INFORMATION:
APPLICANT: Michael W. Glynn
TITLE OF INVENTION: DNA and amino acid sequence specific for natural killer cells
TITLE OF INVENTION: natural killer cells
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
ADDRESSEE: No. 6262244artis Corporation
STREET: 564 Morris Avenue
CITY: Summit,
STATE: NJ
COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514

FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
TELEPHONE: 908-522-6927
TELEFAX: 908-522-6955
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-543-246B-11

Alignment Scores:
Pred. No.: 8.29 Length: 699
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-11 (1-699)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 355 TGTCCTGAGAGTGGATTACATATCCACAGTTGTAT 393

RESULT 10

US-09-591-435-9
Sequence 9, Application US/09591435
Patent No. 6280953
GENERAL INFORMATION:
APPLICANT: SIKELA, JAMES M
TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL AND MEDICAL CONDITIONS
TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL AND MEDICAL CONDITIONS
FILE REFERENCE: GENO.200.2
CURRENT APPLICATION NUMBER: US/09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/591,435
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/240,915
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,263
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/098,987
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 1212
TYPE: DNA
ORGANISM: Homo sapiens
US-09-591-435-9

Alignment Scores:
Pred. No.: 16.5 Length: 1212
Score: 52.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-09-591-435-9 (1-1212)

QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14

```
Db      766 TGCCCTGGGAATGGACATCTTCCAGGAAGAACTGTAC 804
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
US-09-591-435-11
RESULT 11
US-09-591-435-10
; Sequence 10, Application US/09591435
; Patent No. 6280953
; GENERAL INFORMATION:
; APPLICANT: MESSIER, WALTER
; APPLICANT: SIKELA, JAMES M
; TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLEOTIDE AND POLYPEPTIDE
; TITLE OF INVENTION: SEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL
; TITLE OF INVENTION: AND MEDICAL CONDITIONS
; FILE REFERENCE: GENO.200.2
; CURRENT APPLICATION NUMBER: US/09/591,435
; CURRENT FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/591,435
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/240,915
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,263
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/098,987
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Pan troglodytes
US-09-591-435-10
Alignment Scores:
Pred. No.: 16.5 Length: 1212
Score: 52.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 48.15% Indels: 0
Gaps: 3
Db      766 TGCCCTGGGAATGGACATCTTCCAGGAAGAACTGTAC 804
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
US-09-591-435-10 (1-17) x US-09-591-435-10 (1-1212)
QY      2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      766 TGCCCTGGGAATGGACATCTTCCAGGAAGAACTGTAC 804
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
US-09-938-114-4 (1-17) x US-09-591-435-11 (1-1212)
QY      2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      766 TGCCCTGGGAATGGACATCTTCCAGGAAGAACTGTAC 804
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
US-09-938-114-4 (1-17) x US-09-591-435-11 (1-1212)
RESULT 13
US-08-543-246B-5
; Sequence 5, Application US/08543246B
; Patent No. 6262244
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA and amino acid sequence specific for
; TITLE OF INVENTION: natural killer cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Michael W. Glynn
; ADDRESSEE: No. 6262244artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit,
; STATE: NJ
; COUNTRY: US
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/543,246B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,663
; FILING DATE: 28-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02469
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/122,514
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn M.
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 118-7704/PCT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-522-6927
; TELEFAX: 908-522-6955
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1222 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 8..700
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 8..700
; US-08-543-246B-5
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Alignment Scores:
Pred. No.: 16.7 Length: 1222
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 3 Gaps: 0

US-09-938-114-4 (1-17) x US-08-543-246B-5 (1-1222)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 356 TGCTCTGAGGAGTGATTACATATTCACACAGTTGTTAT 394

RESULT 14
US-09-016-434-1347
; Sequence 1347, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G35060
US-09-016-434-1347

Alignment Scores:
Pred. No.: 16.7 Length: 1223
Score: 52.00 Matches: 7
Percent Similarity: 61.54% Conservative: 1
Best Local Similarity: 53.85% Mismatches: 5
Query Match: 48.15% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-016-434-1347 (1-1223)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 356 TGCTCTGAGGAGTGATTACATATTCACACAGTTGTTAT 394

RESULT 15
US-09-517-605-1
; Sequence 1, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(1253)
US-09-517-605-1

Alignment Scores:
Pred. No.: 18.3 Length: 1312
Score: 52.00 Matches: 7
Percent Similarity: 76.92% Conservative: 3
Best Local Similarity: 53.85% Mismatches: 3
Query Match: 48.15% Indels: 0
DB: 4 Gaps: 0

US-09-938-114-4 (1-17) x US-09-517-605-1 (1-1312)

Qy 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
Db 807 TGCTCTGAGGAGTGACATCTTCCAGGAACCTGTAC 845

Search completed: December 8, 2003, 17:27:05
Job time : 15.4057 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 16:08:50 ; Search time 67.6114 Seconds
(without alignments)
835.675 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYEGFCYKFF 17

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2201672 segs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=FastCap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZB=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0938114 -cgn 1_1_504 -runat_08122003_091002_22963
-NCPUS=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US09H_PUBCOMB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
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17:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
18:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	83	76.9	690	10	US-09-969-763-2	Sequence 2, Appli
2	78	72.2	483	10	US-09-929-230-1	Sequence 1, Appli
3	78	72.2	483	13	US-10-226-420-1	Sequence 1, Appli
4	71	65.7	721	10	US-09-929-230-4	Sequence 4, Appli
5	71	65.7	721	13	US-10-226-420-4	Sequence 4, Appli
6	66	61.1	453	10	US-09-929-230-3	Sequence 3, Appli
7	66	61.1	453	13	US-10-226-420-3	Sequence 3, Appli
8	66	61.1	580	10	US-09-929-230-7	Sequence 7, Appli
9	66	61.1	580	13	US-10-226-420-7	Sequence 7, Appli
10	61	56.5	5185	10	US-09-870-759-94	Sequence 94, Appli
11	61	56.5	5185	13	US-09-751-708A-9	Sequence 94, Appli
12	60	55.6	432	10	US-09-929-230-9	Sequence 9, Appli
13	60	55.6	432	13	US-10-226-420-9	Sequence 9, Appli
14	58	53.7	618	9	US-09-764-870-37	Sequence 37, Appli
15	58	53.7	618	15	US-10-125-540-37	Sequence 37, Appli
16	58	53.7	1355	10	US-09-978-295A-230	Sequence 230, App
17	58	53.7	1355	10	US-09-978-697-230	Sequence 230, App
18	58	53.7	1355	10	US-09-978-192A-230	Sequence 230, App
19	58	53.7	1355	10	US-09-999-832A-230	Sequence 230, App
20	58	53.7	1355	11	US-09-978-189-230	Sequence 230, App
21	58	53.7	1355	11	US-09-978-608A-230	Sequence 230, App
22	58	53.7	1355	11	US-09-978-585A-230	Sequence 230, App
23	58	53.7	1355	11	US-09-978-191A-230	Sequence 230, App
24	58	53.7	1355	11	US-09-978-403A-230	Sequence 230, App
25	58	53.7	1355	11	US-09-978-544A-230	Sequence 230, App
26	58	53.7	1355	11	US-09-999-833A-230	Sequence 230, App
27	58	53.7	1355	11	US-09-981-915A-230	Sequence 230, App
28	58	53.7	1355	11	US-09-978-824-230	Sequence 230, App
29	58	53.7	1355	11	US-09-918-585A-230	Sequence 230, App
30	58	53.7	1355	11	US-09-978-423A-230	Sequence 230, App
31	58	53.7	1355	11	US-09-978-193A-230	Sequence 230, App
32	58	53.7	1355	11	US-09-999-830A-230	Sequence 230, App
33	58	53.7	1355	11	US-09-978-757A-230	Sequence 230, App
34	58	53.7	1355	11	US-09-978-187B-230	Sequence 230, App
35	58	53.7	1355	11	US-09-978-643A-230	Sequence 230, App
36	58	53.7	1355	13	US-09-978-375A-230	Sequence 230, App
37	58	53.7	1355	13	US-09-978-188A-230	Sequence 230, App
38	58	53.7	1355	13	US-09-978-298A-230	Sequence 230, App
39	58	53.7	1355	13	US-10-137-870-421	Sequence 421, App
40	58	53.7	1355	13	US-10-140-018-421	Sequence 421, App
41	58	53.7	1355	13	US-10-140-021-421	Sequence 421, App
42	58	53.7	1355	13	US-10-140-274-421	Sequence 421, App
43	58	53.7	1355	13	US-10-140-471-421	Sequence 421, App
44	58	53.7	1355	13	US-10-140-807-421	Sequence 421, App
45	58	53.7	1355	13	US-10-140-922-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-09-969-763-2
; Sequence 2, Application US/09969763
; Publication No. US20020198363A1
; GENERAL INFORMATION:
; APPLICANT: FUKUCHI, NAOKYUKI
; APPLICANT: KITO, MORIKAZU
; APPLICANT: KAYAHARA, TAKASHI
; APPLICANT: FUTAKI, FUMIE
; APPLICANT: ISHIKAWA, KOHKI
; APPLICANT: SUZUKI, EIICHIRO
; APPLICANT: GONDOH, KEIKO
; APPLICANT: SHIMBA, NOBUHISA
; APPLICANT: YAMADA, NAOKYUKI
; TITLE OF INVENTION: PROTEIN HAVING ANTITHROMBOTIC ACTIVITY AND METHOD FOR PRODUCING IT
; FILE REFERENCE: 214760US0
; CURRENT APPLICATION NUMBER: US/09/969,763
; CURRENT FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: JP 2000-305279
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690

; TYPE: DNA
; ORGANISM: Crotales harridus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(512)
; OTHER INFORMATION:
US-09-969-763-2

Alignment Scores:
Pred. No.: 7.15e-05 Length: 690
Score: 83.00 Matches: 12
Percent Similarity: 88.24% Conservatives: 3
Best Local Similarity: 70.59% Mismatches: 2
Query Match: 76.85% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-969-763-2 (1-690)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
Db 141 GAATGTCCTCCGGTGGTCTCTATGATCGGTATGCTACAGCCCTTC 191

RESULT 2

US-09-929-230-1
; Sequence 1, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(455)
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk2
US-09-929-230-1

Alignment Scores:
Pred. No.: 0.000342 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservatives: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-1 (1-483)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
Db 60 GATTGTCCTCTGACTGGTCTCTATGATCAGCATGCTACAGGCTTC 110

RESULT 3

US-10-226-420-1
; Sequence 1, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 483

; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(455)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk2
US-10-226-420-1

Alignment Scores:
Pred. No.: 0.000342 Length: 483
Score: 78.00 Matches: 12
Percent Similarity: 82.35% Conservatives: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 72.22% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-10-226-420-1 (1-483)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
Db 60 GATTGTCCTCTGACTGGTCTCTATGATCAGCATGCTACAGGCTTC 110

RESULT 4

US-09-929-230-4
; Sequence 4, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)...(546)
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Zsnk3
US-09-929-230-4

Alignment Scores:
Pred. No.: 0.00873 Length: 721
Score: 71.00 Matches: 11
Percent Similarity: 76.47% Conservatives: 2
Best Local Similarity: 64.71% Mismatches: 4
Query Match: 65.74% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-4 (1-721)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
Db 160 GATTGTCCTCTGCTGCTCTATGATCAGCATGCTACAGGCTTC 210

RESULT 5

US-10-226-420-4
; Sequence 4, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.


```

; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)...(546)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk3
US-10-226-420-4
Alignment Scores:
Pred. No.: 0.00873
Score: 71.00
Percent Similarity: 76.47%
Best Local Similarity: 64.71%
Query Match: 65.74%
DB: 13
US-09-938-114-4 (1-17) x US-10-226-420-4 (1-721)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 160 GATTGTCCTCTGGTGGTCTCTATGATCAGCATTCGCTACAGGTCCTTC 210
RESULT 6
US-09-929-230-3
; Sequence 3, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.

```

```

; NAME/KEY: misc feature
; LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
; LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
; LOCATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222,
; LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
; LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
; OTHER INFORMATION: n = A,T,C or G
US-09-929-230-3
Alignment Scores:
Pred. No.: 0.0368
Score: 66.00
Percent Similarity: 64.71%
Best Local Similarity: 52.94%
Query Match: 61.11%
DB: 10
US-09-929-230-3
; Sequence 3, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc feature
; LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
; LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
; LOCATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222,
; LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
; LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
; OTHER INFORMATION: n = A,T,C or G
US-09-929-230-3
Alignment Scores:
Pred. No.: 0.0368
Score: 66.00
Percent Similarity: 64.71%
Best Local Similarity: 52.94%
Query Match: 61.11%
DB: 10

```

```

US-09-938-114-4 (1-17) x US-09-929-230-3 (1-453)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 58 GAYTGYCCNWSNGAYTGGWSNWSNTAIGAYCARCAYTGTYATAARGTNTTY 108
RESULT 7
US-10-226-420-3
; Sequence 3, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:2.
; NAME/KEY: misc feature
; LOCATION: 9, 12, 18, 21, 24, 27, 30, 36, 39, 42, 45, 48, 51, 54, 57,
; LOCATION: 66, 69, 78, 81, 105, 111, 117, 123, 135, 141, 153, 162,
; LOCATION: 168, 171, 174, 177, 180, 189, 192, 204, 210, 213, 219, 222,
; LOCATION: 225, 231, 234, 243, 246, 258, 261, 270, 297, 306, 312, 324
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 330, 333, 336, 339, 348, 351, 357, 360, 366, 372, 390, 393,
; LOCATION: 405, 408, 411, 417, 432, 435, 438, 441, 447, 450, 453
; OTHER INFORMATION: n = A,T,C or G
US-10-226-420-3
Alignment Scores:
Pred. No.: 0.0368
Score: 66.00
Percent Similarity: 64.71%
Best Local Similarity: 52.94%
Query Match: 61.11%
DB: 13
US-09-938-114-4 (1-17) x US-10-226-420-3 (1-453)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 58 GAYTGYCCNWSNGAYTGGWSNWSNTAIGAYCARCAYTGTYATAARGTNTTY 108
RESULT 8
US-09-929-230-7
; Sequence 7, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:

```

```
; NAME/KEY: CDS
; LOCATION: (3)...(434)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk4
US-09-929-230-7

Alignment Scores:
Pred. No.: 0.0491 Length: 580
Score: 66.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 61.11% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-7 (1-580)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 36 GATTGTCCTCTGATTGGTATGCGTATGATCAGTATTGCTACAGG 80

RESULT 9
US-10-226-420-7
; Sequence 94, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sistrurus miliarius
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(434)
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Zsnk4
US-10-226-420-7

Alignment Scores:
Pred. No.: 0.0491 Length: 580
Score: 66.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 61.11% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-10-226-420-7 (1-580)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 36 GATTGTCCTCTGATTGGTATGCGTATGATCAGTATTGCTACAGG 80

RESULT 10
US-09-870-759-94
; Sequence 94, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
```

```
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(4474)
; OTHER INFORMATION:
US-09-870-759-94

Alignment Scores:
Pred. No.: 4.59 Length: 5185
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 56.48% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-870-759-94 (1-5185)
QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 1187 TGTCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACAAG 1228

RESULT 11
US-09-751-708A-94
; Sequence 94, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)...(4474)
; OTHER INFORMATION:
US-09-751-708A-94

Alignment Scores:
Pred. No.: 4.59 Length: 5185
Score: 61.00 Matches: 9
Percent Similarity: 71.43% Conservative: 1
Best Local Similarity: 64.29% Mismatches: 4
Query Match: 56.48% Indels: 0
DB: 13 Gaps: 0

US-09-938-114-4 (1-17) x US-09-751-708A-94 (1-5185)
QY 2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyrLys 15
Db 1187 TGTCTAGTCAGTGGTGGCGGTATGCGGTCACTGTTACAAG 1228

RESULT 12
US-09-929-230-9
; Sequence 94, Application US/09929230
; Patent No. US20020161203A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
```

; CURRENT APPLICATION NUMBER: US/09/929,230
; CURRENT FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
; NAME/KEY: misc feature
; LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111,
; LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180,
; LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276,
; LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
; OTHER INFORMATION: n = A,T,C or G
US-09-929-230-9

Alignment Scores:
Pred. No.: 0.374 Length: 432
Score: 60.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 55.56% Indels: 0
DB: 10 Gaps: 0

US-09-938-114-4 (1-17) x US-09-929-230-9 (1-432)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAY 75

RESULT 13
US-10-226-420-9
; Sequence 9, Application US/10226420
; Publication No. US20030157686A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
; FILE REFERENCE: 00-72
; CURRENT APPLICATION NUMBER: US/10/226,420
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: This degenerate nucleotide sequence encodes the
; OTHER INFORMATION: amino acid sequence of SEQ ID NO:8.
; NAME/KEY: misc feature
; LOCATION: 6, 15, 18, 21, 24, 27, 42, 45, 57, 78, 81, 93, 96, 99, 111,
; LOCATION: 117, 126, 135, 141, 144, 150, 153, 156, 165, 171, 177, 180,
; LOCATION: 186, 189, 195, 198, 201, 231, 240, 243, 246, 255, 273, 276,
; LOCATION: 285, 291, 294, 297, 300, 315, 327, 330, 345, 348, 360
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: 363, 369, 372, 378, 384, 393, 405, 423, 426
; OTHER INFORMATION: n = A,T,C or G
US-10-226-420-9

Alignment Scores:
Pred. No.: 0.374 Length: 432
Score: 60.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4

Best Local Similarity: 50.00% Mismatches: 3
Query Match: 55.56% Indels: 0
DB: 13 Gaps: 0
US-09-938-114-4 (1-17) x US-10-226-420-9 (1-432)
QY 1 AspCysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 34 GAYTGYCCNWSNGAYTGGTAYGCNTAYGAYCARTAYTGYTAY 75

RESULT 14
US-09-764-870-37
; Sequence 37, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (598)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-870-37

Alignment Scores:
Pred. No.: 1.26 Length: 618
Score: 58.00 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 3
Query Match: 53.70% Indels: 0
DB: 9 Gaps: 0

US-09-938-114-4 (1-17) x US-09-764-870-37 (1-618)
QY 2 CysProSerGluTrpSerSerTyrrGluGlyPheCysTyr 14
Db 247 TGCCCCACGTGGTGGTCTTCGAGGGGCTCCTGCTAC 285

RESULT 15
US-10-125-540-37
; Sequence 37, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ14C1
; CURRENT APPLICATION NUMBER: US/10/125,540
; CURRENT FILING DATE: 2002-04-19
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37

Tue Dec 9 09:26:59 2003

```

; LENGTH: 618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (48)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (588)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (598)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-125-540-37

```

```

Alignment Scores:
Pred. No.: 1.26 Length: 618
Score: 58.00 Matches: 8
Percent Similarity: 76.92% Conservative: 2
Best Local Similarity: 61.54% Mismatches: 3
Query Match: 53.70% Indels: 0
DB: 15 Gaps: 0

```

US-09-938-114-4 (1-17) x US-10-125-540-37 (1-618)

```

Qy      2 CysProSerGluTrpSerSerTyrGluGlyPheCysTyr 14
         |||||::: |||||
Db      247 TGCCCCACGTCGTGGCTGCTTCGAGGGCTCCTGCTAC 285

```

Search completed: December 8, 2003, 19:36:07
Job time : 69.6114 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:49:54 ; Search time 3.4 Seconds
(without alignments)
480.843 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSSYEGFCYKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	101	93.5	146	2	JC71135	agkisacutacin beta
2	98	90.7	146	2	JC4691	coagulation factor
3	94	87.0	129	2	JC4329	coagulation factor
4	94	87.0	146	2	JC7105	aggregin beta chain
5	84	77.8	30	2	B53088	factor IX/factor X
6	82	75.9	40	2	S56006	tokaracetin alpha
7	81	75.0	30	2	A53088	factor IX/factor X
8	81	75.0	133	2	A47267	botrocetin alpha c
9	79	73.1	125	2	B47267	botrocetin alpha c
10	77	71.3	40	2	A56829	alboaggregin-B bet
11	77	71.3	152	2	JC71134	agkisacutacin alph
12	76	70.4	152	2	JC4690	coagulation factor
13	75	69.4	40	2	S56007	tokaracetin beta c
14	71	65.7	123	2	B42972	coagulation factor
15	69	63.9	40	2	B56829	alboaggregin-B alp
16	67	62.0	123	2	JC2415	echicetin beta cha
17	64	59.3	125	2	JC5058	bitiscetin beta ch
18	64	59.3	131	2	JC5058	bitiscetin alpha c
19	62	57.4	29	2	PC4421	multicativase (EC 3
20	61	56.5	1456	1	A36583	mannose receptor p
21	58	53.7	16	2	A48630	bothrojaracin - ja
22	58	53.7	71	2	S55679	flavocetin A - hab
23	55	50.9	284	1	LNRTL	hepatic lectin - r
24	55	50.9	284	2	S29855	asialoglycoprotein
25	55	50.9	1455	1	A48925	mannose receptor p
26	54	50.0	46	2	FX0080	lectin SPL-2, Ca2+
27	54	50.0	135	2	A38609	lectin, galactose-
28	54	50.0	2415	1	A39086	aggreacan precursor
29	53	49.1	143	2	D71009	hypothetical prote

ALIGNMENTS

RESULT 1

JC71135

agkisacutacin beta chain precursor - sharp-nosed viper

N/Alternate names: fibrinogenolytic venom protein

C/Species: Agkistrodon acutus (sharp-nosed viper)

C/Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000

C/Accession: JC71135; PC7038

R/Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A/Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom

A/Reference number: JC71134; MUID:20025379; PMID:10558903

A/Accession: JC71135

A/Molecule type: mRNA

A/Residues: 1-146 <CH>

A/Cross-references: GB:AF176421

A/Experimental source: venom gland

A/Accession: PC7038

A/Molecule type: protein

A/Residues: 24-50;59-83;102-107;112-114 <CH2>

C/Superfamily: tetranectin; C-type lectin homology

C/Keywords: disulfide bond; heterodimer; venom

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-146/Product: agkisacutacin beta chain #status experimental <MAT>

Query Match

Best Local Similarity 93.5%; Score 101; DB 2; Length 146;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17

Db 24 DCPSEWSSYEGHCYKPF 40

RESULT 2

JC4691

coagulation factor IX/factor X-binding protein chain A precursor - habu

C/Species: Trimeresurus flavoviridis (habu)

C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000

C/Accession: JC4691; B39332; JC4330

R/Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.

Biochem. Biophys. Res. Commun. 220, 382-387, 1996

A/Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from sr

A/Reference number: JC4690; MUID:96184662; PMID:8645314

A/Accession: JC4691

A/Molecule type: mRNA

A/Residues: 1-146 <MAT1>

A/Cross-references: DDBJ:D83332; NID:gl402641; PIDN:BAAL1888.1; PID:gl402642

A/Experimental source: venom

R/Atoda, H.; Hyuga, M.; Morita, T.

J. Biol. Chem. 266, 14903-14911, 1991

A/Title: The primary structure of coagulation factor IX/factor X-binding protein isolates: otein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.

A;Reference number: A39332; MUID:91332000; PMID:1831197
 A;Accession: B39332
 A;Molecule type: protein
 A;Residues: 24-146 <ATO>
 R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
 J. Biochem. 118, 965-973, 1995
 A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavoviridis
 A;Reference number: JC4329; MUID:96318509; PMID:8749314
 A;Accession: JC4330
 A;Molecule type: protein
 A;Residues: 24-146 <AT2>
 C;Superfamily: tetranectin; C-type lectin homology
 C;Keywords: anticoagulant; blood coagulation; lectin; venom
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-146/Product: factor IX/X binding protein chain B #status predicted <MAT>
 F;25-142/Domain: C-type lectin homology <LCH>
 F;25-36,53-142,119-134/Disulfide bonds: #status predicted

Query Match 90.7%; Score 98; DB 2; Length 146;
 Best Local Similarity 88.2%; Pred. No. 1.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||| ||||| |||||
 DB 24 DCPSDWSSYEGHCYKPF 40

RESULT 3
 JC4329
 coagulation factor IX-binding protein A chain - habu
 C;Species: Trimeresurus flavoviridis (habu)
 C;Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 13-Mar-1998
 C;Accession: JC4329
 R;Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
 J. Biochem. 118, 965-973, 1995
 A;Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus flavoviridis
 A;Reference number: JC4329; MUID:96318509; PMID:8749314
 A;Accession: JC4329
 A;Molecule type: protein
 A;Residues: 1-129 <ATO>
 C;Comment: This protein binds calcium.
 C;Superfamily: tetranectin; C-type lectin homology
 C;Keywords: anticoagulant; blood coagulation; calcium binding; venom
 F;2-127/Domain: C-type lectin homology <LCH>
 F;2-13,30-127,102-119/Disulfide bonds: #status predicted

Query Match 87.0%; Score 94; DB 2; Length 129;
 Best Local Similarity 88.2%; Pred. No. 3.5e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||| ||||| |||||
 DB 1 DCPSGWSSYEGHCYKPF 17

RESULT 4
 JC7105
 aggrexin beta chain - Malayan pit viper
 C;Species: Calloselasma rhodostoma (Malayan pit viper)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
 C;Accession: JC7105
 R;Chung, C.H.; Au, L.C.; Huang, T.F.
 Biochem. Biophys. Res. Commun. 263, 723-727, 1999
 A;Title: Molecular cloning and sequence analysis of aggrexin, a collagen-like platelet alpha 2(IIb) glycoprotein
 A;Reference number: PC7027; MUID:99443731; PMID:10512747
 A;Accession: JC7105
 A;Molecule type: mRNA
 A;Residues: 1-146 <CHU>
 A;Experimental source: venom gland
 C;Superfamily: tetranectin; C-type lectin homology
 C;Keywords: disulfide bond; platelet aggregation; venom

Query Match 87.0%; Score 94; DB 2; Length 146;

Best Local Similarity 88.2%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||| ||||| |||||
 DB 24 DCPSGWSSYEGHCYKPF 40

RESULT 5
 B53088
 factor IX/factor X-binding anticoagulant protein A chain - jararaca (fragment)
 C;Species: Bothrops jararaca (jararaca)
 C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
 C;Accession: B53088
 R;Sekiya, F.; Atoda, H.; Morita, T.
 Biochemistry 32, 6892-6897, 1993
 A;Title: Isolation and characterization of an anticoagulant protein homologous to botrocetin
 A;Reference number: A53088; MUID:93326575; PMID:8334120
 A;Accession: B53088
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-30 <SEK>
 A;Experimental source: venom
 A;Note: sequence extracted from NCBI backbone (NCBIP:135336)

Query Match 77.8%; Score 84; DB 2; Length 30;
 Best Local Similarity 76.5%; Pred. No. 2.7e-05;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||| ||||| |||||
 DB 1 DCPSDWSSYEGHCYKPF 17

RESULT 6
 S56006
 tokaracetin alpha chain - Trimeresurus tokarensis (fragment)
 N;Alternate names: platelet aggregation inhibitor; platelet antagonist
 C;Species: Trimeresurus tokarensis
 C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
 C;Accession: S56006
 R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, K.; Sakai, M.
 Biochem. J. 308, 947-953, 1995
 A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib alpha
 A;Reference number: S56006; MUID:97104297; PMID:8948455
 A;Accession: S56006
 A;Molecule type: protein
 A;Residues: 1-40 <KAW>
 C;Superfamily: tetranectin; C-type lectin homology

Query Match 75.9%; Score 82; DB 2; Length 40;
 Best Local Similarity 70.6%; Pred. No. 6.5e-05;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 ||||| ||||| |||||
 DB 1 DCPSGWSSYEGHCYKPF 17

RESULT 7
 A53088
 factor IX/factor X-binding anticoagulant protein B chain - jararaca (fragment)
 C;Species: Bothrops jararaca (jararaca)
 C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
 C;Accession: A53088
 R;Sekiya, F.; Atoda, H.; Morita, T.
 Biochemistry 32, 6892-6897, 1993
 A;Title: Isolation and characterization of an anticoagulant protein homologous to botrocetin
 A;Reference number: A53088; MUID:93326575; PMID:8334120
 A;Accession: A53088
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-30 <SEK>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:135337)

Query Match 75.0%; Score 81; DB 2; Length 30;

Best Local Similarity 70.6%; Pred. No. 7e-05;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPSDWSPYEGHCYRVF 17

RESULT 8

A47267

botroctetin alpha chain - jararaca

N;Alternate names: two chain botrocetin alpha chain

C;Species: Bothrops jararaca (jararaca)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998

C;Accession: A47267; B37958

R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu

A;Reference number: A47267; MUID:93157385; PMID:8430107

A;Accession: A47267

A;Molecule type: protein

A;Residues: 1-133 <USA>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:124085)

R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug

Biochemistry 30, 1957-1964, 1991

A;Title: Isolation and chemical characterization of two structurally and functionally di

A;Reference number: A37958; MUID:91129280; PMID:1993206

A;Accession: B37958

A;Molecule type: protein

A;Residues: 1-40 <FUJ>

C;Complex: heterodimer of alpha and beta (see PIR:B47267) chains

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: hemagglutinin; heterodimer; venom

F;2-128/Domain: C-type lectin homology <LCH>

F;2-13,30-128,103-120/Disulfide bonds: #status experimental

F;80/Disulfide bonds: interchain (to beta-75) #status experimental

Query Match 75.0%; Score 81; DB 2; Length 133;

Best Local Similarity 82.4%; Pred. No. 0.00024;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPSGWSSYEGHCYKPF 17

RESULT 9

B47267

botroctetin beta chain - jararaca

N;Alternate names: two chain botrocetin beta chain

C;Species: Bothrops jararaca (jararaca)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998

C;Accession: B47267; C37958

R;Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator pu

A;Reference number: A47267; MUID:93157385; PMID:8430107

A;Accession: B47267

A;Molecule type: protein

A;Residues: 1-125 <USA>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:124086)

R;Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug

Biochemistry 30, 1957-1964, 1991

A;Title: Isolation and chemical characterization of two structurally and functionally di

A;Reference number: A37958; MUID:91129280; PMID:1993206

A;Accession: C37958

A;Molecule type: protein

A;Residues: 1-40 <FUJ>

C;Complex: heterodimer of alpha (see PIR:A47267) and beta chains

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: hemagglutinin; heterodimer; venom

F;2-121/Domain: C-type lectin homology <LCH>

F;2-13,30-121,98-113/Disulfide bonds: #status experimental

F;75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 73.1%; Score 79; DB 2; Length 125;

Best Local Similarity 70.6%; Pred. No. 0.00043;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPDWSYEGHCYRVF 17

RESULT 10

A56829

alboaggregin-B beta chain - green pit viper (fragment)

C;Species: Trimeresurus albolabris (green pit viper)

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C;Accession: A56829

R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.; S

Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993

A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous a

A;Reference number: A56829; MUID:93221514; PMID:8466514

A;Accession: A56829

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-40 <YOS>

A;Experimental source: venom

A;Note: sequence extracted from NCBI backbone (NCBIP:128750)

C;Keywords: disulfide bond; heterodimer

Query Match 71.3%; Score 77; DB 2; Length 40;

Best Local Similarity 64.7%; Pred. No. 0.00032;

Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 1 DCPDWSYDYLCYRVF 17

RESULT 11

JC7134

agkisacutacin alpha chain precursor - sharp-nosed viper

N;Alternate names: fibrinogenolytic venom protein

C;Species: Agkistrodon acutus (sharp-nosed viper)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 24-Oct-2000

C;Accession: JC7134; PC7037

R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

Biochem. Biophys. Res. Commun. 265, 530-535, 1999

A;Title: Purification, characterization, and cDNA cloning of a new fibrinogenolytic venom

A;Reference number: JC7134; MUID:20025379; PMID:10558903

A;Accession: JC7134

A;Molecule type: mRNA

A;Residues: 1-152 <CHE>

A;Cross-references: GB:AF176420

A;Experimental source: venom gland

A;Accession: PC7037

A;Molecule type: protein

A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>

C;Superfamily: tetranectin; C-type lectin homology

C;Keywords: disulfide bond; heterodimer; venom

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-152/Product: agkisacutacin alpha chain #status experimental <MAT>

Query Match 71.3%; Score 77; DB 2; Length 152;

Best Local Similarity 76.5%; Pred. No. 0.00097;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17

Db 24 DCSSGWSYEGHCYKVF 40
|| | ||||| ||| |

RESULT 12

JC4690
coagulation factor IX/factor X-binding protein chain A precursor - habu
C;Species: Trimeresurus flavoviridis (habu)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Jun-2000
C;Accession: JC4690; A39332
R;Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
Biochem. Biophys. Res. Commun. 220, 382-387, 1996
A;Title: cDNA cloning of IX/X-BF, a heterogeneous two-chain anticoagulant protein from s
A;Reference number: JC4690; MUID:96184662; PMID:8645314
A;Accession: JC4690
A;Molecule type: mRNA
A;Residues: 1-152 <MAT1>
A;Cross-references: DDBJ:D83331; NID:gl402639; PIDN:BAA11887.1; PID:gl402640
A;Experimental source: venom
R;Atoda, H.; Hyuga, M.; Morita, T.
J. Biol. Chem. 266, 14903-14911, 1991
A;Title: The primary structure of coagulation factor IX/factor X-binding protein isolate
otein, tetranectin, and lymphocyte FC epsilon receptor for immunoglobulin E.
A;Reference number: A39332; MUID:91332000; PMID:1831197
A;Accession: A39332
A;Status: preliminary
A;Molecule type: protein
A;Residues: 24-152 <ATO>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: anticoagulant; blood coagulation; glycoprotein; hemolymph; lectin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-152/Product: factor IX/X binding protein chain A #status predicted <MAT>
F;25-150/Domain: C-type lectin homology <LCH>
F;25-36,53-150,125-142/Disulfide bonds: #status predicted

Query Match 70.4%; Score 76; DB 2; Length 152;
Best Local Similarity 76.5%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 24 DCUSGWSYEGHCYKVF 40

RESULT 13

S56007
tokaracetin beta chain - Trimeresurus tokarensis (fragment)
N;Alternate names: platelet aggregation inhibitor; platelet antagonist
C;Species: Trimeresurus tokarensis
C;Date: 10-Oct-1995 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: S56007
R;Kawasaki, T.; Taniuchi, Y.; Hisamichi, N.; Fujimura, Y.; Suzuki, M.; Titani, K.; Sakai
Biochem. J. 308, 947-953, 1995
A;Title: Tokaracetin, a new platelet antagonist that binds to platelet glycoprotein Ib a
A;Reference number: S56006; MUID:97104297; PMID:8948455
A;Accession: S56007
A;Molecule type: protein
A;Residues: 1-40 <KAW>

Query Match 69.4%; Score 75; DB 2; Length 40;
Best Local Similarity 64.7%; Pred. No. 0.00062;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 1 DCPFDWSSYDEHCYRVF 17

RESULT 14

B42972
coagulation factor X activating enzyme (EC 3.4.24.-) light chain - Russell's viper
C;Species: Vipera russelli (Russell's viper)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997

C;Accession: B42972
R;Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
J. Biol. Chem. 267, 14109-14117, 1992
A;Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A no
A;Reference number: A42972; MUID:92332516; PMID:1629211
A;Contents: V. r. siamensis
A;Accession: B42972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <TAK>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:108408)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;4-121/Domain: C-type lectin homology <LCH>
F;4-15,32-121,98-113/Disulfide bonds: #status predicted

Query Match 65.7%; Score 71; DB 2; Length 123;
Best Local Similarity 70.6%; Pred. No. 0.0056;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
|| | ||||| ||| |
Db 3 DCPSGWLSYEGHCYKGF 19

RESULT 15

B56829
alboaggregin-B alpha chain - green pit viper (fragment)
C;Species: Trimeresurus albolabris (green pit viper)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 03-May-1996
C;Accession: B56829
R;Yoshida, E.; Fujimura, Y.; Miura, S.; Sugimoto, M.; Fukui, H.; Narita, N.; Usami, Y.;
Biochem. Biophys. Res. Commun. 191, 1386-1392, 1993
A;Title: Alboaggregin-B and botrocetin, two snake venom proteins with highly homologous
A;Reference number: A56829; MUID:93221514; PMID:8466514
A;Accession: B56829
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <YOS>
A;Experimental source: venom
A;Note: sequence extracted from NCBI backbone (NCBIP:128751)
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer

Query Match 63.9%; Score 69; DB 2; Length 40;
Best Local Similarity 60.0%; Pred. No. 0.0042;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYK 15
|| | ||||| ||| |
Db 1 DCFSDWSSFKQYCYQ 15

Search completed: December 8, 2003, 09:55:35
Job time : 3.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:46:14 ; Search time 2.23429 Seconds
(without alignments)
357.812 Million cell updates/sec

Title: US-09-938-114-4

Perfect score: 108

Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	98	90.7	146	1	IXB_TRIFL
2	86	79.6	117	1	CHBB_CROHO
3	86	79.6	123	1	ABA4_TRIAB
4	83	76.9	127	1	CHBA_CROHO
5	81	75.0	133	1	BOTA_BOTJA
6	80	74.1	118	1	ABBB_TRIAB
7	80	74.1	125	1	ABAB_TRIAB
8	79	73.1	131	1	BOTB_BOTJA
9	79	73.1	131	1	ABAL_TRIAB
10	76	70.4	152	1	IXA_TRIFL
11	74	68.5	148	1	CVXB_CRODU
12	72	66.7	133	1	RHCA_AGRKH
13	69	63.9	132	1	ABBA_TRIAB
14	67	62.0	123	1	ECHE_ECHCA
15	64	59.3	129	1	RHCB_AGRKH
16	64	59.3	133	1	ECBA_ECHCA
17	62	57.4	29	1	MULR_ECHML
18	61	56.5	1456	1	MANR_HUMAN
19	56	51.9	158	1	CVXA_CRODU
20	55	50.9	283	1	LECH_MOUSE
21	55	50.9	283	1	LECH_RAT
22	54	50.0	135	1	LECG_CROAT
23	54	50.0	2415	1	PGCA_HUMAN
24	53	49.1	304	1	MMGL_MOUSE
25	52	48.1	158	1	NRGF_HUMAN
26	52	48.1	158	1	NRGF_PANTR
27	52	48.1	231	1	NRGC_HUMAN
28	52	48.1	231	1	NRGC_MACMU
29	52	48.1	233	1	NRGA_HUMAN
30	52	48.1	233	1	NRGA_MACMU
31	52	48.1	233	1	NRKA_PANTR
32	52	48.1	240	1	NRKE_HUMAN
33	52	48.1	240	1	NRKE_PANTR

RESULT 1
IXB_TRIFL

ID IXB TRIFL STANDARD; PRT; 146 AA.
AC P23807; Q91247;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX/factor X-binding protein B chain precursor (IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96184662; PubMed=8645314;
RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;
RT "CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
RL Biochem. Biophys. Res. Commun. 220:382-387(1996).
RN [2]
RP SEQUENCE OF 24-146.
RC TISSUE=Venom;
RX MEDLINE=91332000; PubMed=1831197;
RA Atoda H., Hyuga M., Morita T.;
RT "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis. Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin E.";
RL J. Biol. Chem. 266:14903-14911(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=97331317; PubMed=9187649;
RA Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT "Structure of coagulation factors IX/X-binding protein, a heterodimer of C-type lectin domains.";
RL Nat. Struct. Biol. 4:438-441(1997).
CC -|- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC -|- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -|- SIMILARITY: Contains 1 C-type lectin family domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; D83332; BAA11888.1; -;
DR FRC; JC4691; JC4691.

34 51 47.2 134 1 ABA2 TRIAB
35 51 47.2 168 1 VAA0 VACC
36 51 47.2 168 1 VAA0 VACC
37 51 47.2 306 1 MMGL RAT
38 51 47.2 548 1 IDD MOUSE
39 51 47.2 883 1 PGCB MOUSE
40 51 47.2 912 1 PGCB BOVIN
41 50 46.3 167 1 V008 FOWPV
42 50 46.3 2124 1 PGCA RAT
43 50 46.3 2132 1 PGCA BOVIN
44 50 46.3 2364 1 PGCA BOVIN
45 49 45.4 175 1 ANP_OSMO

ALIGNMENTS

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DR PDB; 1LXX; 06-MAY-98.
DR PDB; 1BJ3; 16-AUG-99.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 146
FT DOMAIN 24 144
FT DISULFID 25 36
FT DISULFID 53 142
FT DISULFID 98 98
FT DISULFID 119 134
FT TURN 27 28
FT TURN 30 32
FT TURN 33 34
FT STRAND 35 44
FT STRAND 46 54
FT TURN 55 56
FT TURN 58 59
FT STRAND 61 62
FT HELIX 68 82
FT STRAND 86 88
FT TURN 94 97
FT STRAND 100 102
FT TURN 103 104
FT STRAND 113 113
FT STRAND 118 123
FT TURN 124 125
FT STRAND 126 133
FT TURN 134 135
FT STRAND 138 146
SQ SEQUENCE 146 AA; 16922 MW; 8E1961C59F96757C CRC64;

Query Match 90.7%; Score 98; DB 1; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.8e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
DQ 24 DCPSDWSSYEGHCYKPF 40
||||:|||||

RESULT 2
CHBB CROHO STANDARD; PRT; 117 AA.
AC P81509;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE CH-B beta subunit.
OS Crotalus horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton aldoaggregin from Trimeresurus
RT albopictus and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system, inhibits VWF
CC binding, and stimulates agglutination.
CC -!- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 9 116 C-TYPE LECTIN.
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 115 BY SIMILARITY.
FT DISULFID 92 92 INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
(POTENTIAL).
FT DISULFID 95 107 BY SIMILARITY.
SQ SEQUENCE 117 AA; 13888 MW; 07835BBC61E9EAD CRC64;

Query Match 79.6%; Score 86; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 8e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
DQ 1 DCPSDWSSYEGHCYKRVF 17
||||:|||||

RESULT 3
ABA4 TRIAB STANDARD; PRT; 123 AA.
AC P8114;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 4.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -!- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSPF; P23807; lixx.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 119 BY SIMILARITY.
FT DISULFID 96 111 BY SIMILARITY.
SQ SEQUENCE 123 AA; 14365 MW; D4CFBEE1219C9B1E CRC64;

Query Match 79.6%; Score 86; DB 1; Length 123;
Best Local Similarity 76.5%; Pred. No. 8.4e-06;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DCPSEWSSYEGFCYKPF 17
DQ 1 DCPSDWSSYEGHCYKRVF 17
||||:|||||

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RESULT 4
CHBA_CROHO
ID CHBA_CROHO STANDARD; PRT; 127 AA.
AC P81508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CHB-B alpha subunit.
OS Crotales horridus horridus (Timber rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8747;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=96420502; PubMed=8823201;
RA Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
RA Smith A.I., Lopez J.A., Berndt M.C.;
RT "Binding of a novel 50-kilodalton albosaggregin from Trimeresurus
RT albolabris and related viper venom proteins to the platelet membrane
RT glycoprotein Ib-IX-V complex. Effect on platelet aggregation and
RT glycoprotein Ib-mediated platelet activation.";
RL Biochemistry 35:12629-12639(1996).
CC -1- FUNCTION: Binds to platelet GPIIb/IX receptor system, inhibits VWF
CC -1- binding, and stimulates agglutination.
CC -1- SUBUNIT: Heterodimer of alpha and beta subunits; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR SMART, SM00034; CLECT; 1.
DR PROSITE, PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE, PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 11 121 C-TYPE LECTIN.
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 120 BY SIMILARITY.
FT DISULFID 81 81 INTERCHAIN (WITH C-92 IN BETA CHAIN)
FT DISULFID 95 112 (POTENTIAL).
FT DISULFID 127 AA; 15162 MW; B5DA100D383E3547 CRC64;
SQ SEQUENCE 127 AA; 15162 MW; B5DA100D383E3547 CRC64;

Query Match 76.9%; Score 83; DB 1; Length 127;
Best Local Similarity 70.6%; Pred. No. 2.3e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||:
Db 3 ECPGWSYDYRYCYKPF 19

RESULT 5
BOTA_BOTJA
ID BOTA_BOTJA STANDARD; PRT; 133 AA.
AC P22029;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Botrocetin, alpha chain (platelet coagglutinin).
OC Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
RT modulator purified from the venom of Bothrops jararaca.";

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Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
[2]
RN SEQUENCE OF 1-40.
RP TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
RT functionally distinct forms of botrocetin, the platelet coagglutinin
RT isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=22118144; PubMed=12121649;
RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
RA Liddington R.C.;
RT "Structural basis of von Willebrand factor activation by the snake
RT toxin botrocetin.";
RL Structure 10:943-950(2002).
CC -1- FUNCTION: Two-chain Botrocetin forms an activated complex with
CC VWF, and the complex then binds to platelet GPIb, resulting in
CC platelet agglutination.
CC -1- FUNCTION: There are two distinct forms of the von Willebrand
CC factor-dependent platelet coagglutinin. The dimeric form is
CC 34-times more active than the one-chain Botrocetin in promoting
CC VWF binding to platelets.
CC -1- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC VWF and Botrocetin form a soluble complex.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR PIR, A47267; A47267.
DR PDB; 1JJK; 17-JUL-02.
DR PDB; 1FVU; 14-FEB-01.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEII.
DR SMART, SM00034; CLECT; 1.
DR PROSITE, PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE, PS00041; C_TYPE_LECTIN_2; 1.
KW Lectin; 3D-structure.
FT DISULFID 2 13
FT DISULFID 30 128
FT DISULFID 80 80 INTERCHAIN (WITH C-75 IN BETA CHAIN).
FT DISULFID 103 120
SQ SEQUENCE 133 AA; 15215 MW; E4CF4502946AC74B CRC64;

Query Match 75.0%; Score 81; DB 1; Length 133;
Best Local Similarity 82.4%; Pred. No. 4.8e-05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
:|||||: :|||:
Db 1 DCPSGWSSYEGNYCYKPF 17

RESULT 6
ABBB_TRIAB
ID ABBB_TRIAB STANDARD; PRT; 118 AA.
AC P81116;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin B beta subunit.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;

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RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
CC -1- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 118 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 75 75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)
FT DISULFID 96 111 (BY SIMILARITY).
FT DISULFID 118 AA; 13794 MW; 059EDPF6H474C4CE CRC64;
SQ SEQUENCE 118 AA; 13794 MW; 059EDPF6H474C4CE CRC64;
Query Match 74.1%; Score 80; DB 1; Length 118;
Best Local Similarity 70.6%; Pred. No. 5.9e-05;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
DB 1 DCPSDWSSYDYCYKVF 17
RESULT 7
ABA3 TRIAB STANDARD; PRT; 125 AA.
AC P8113;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 3.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
platelets.";
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DOMAIN 3 123 C-TYPE LECTIN (LONG FORM).
FT DISULFID 4 15 BY SIMILARITY.
FT DISULFID 32 121 BY SIMILARITY.
FT DISULFID 98 113 BY SIMILARITY.
SQ SEQUENCE 125 AA; 14798 MW; CAPA24C098DF3293 CRC64;

Query Match 74.1%; Score 80; DB 1; Length 125;
Best Local Similarity 70.6%; Pred. No. 6.3e-05;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DCPSEWSSYEGFCYKPF 17
DB 3 DCPFGWSSYEGYCYKVY 19
RESULT 8
BOTB BOTJA STANDARD; PRT; 125 AA.
AC P22030;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Botrocetin, beta chain (Platelet coagglutinin).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
modulator purified from the venom of Bothrops jararaca.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN [2]
RP SEQUENCE OF 1-40.
RC TISSUE=Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=22118144; PubMed=12121649;
RA Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
RA Liddington R.C.;
RT "Structural basis of von Willebrand factor activation by the snake
toxin botrocetin.";
RL Structure 10:943-950(2002).
CC -1- FUNCTION: Two-chain Botrocetin forms an activated complex with
vWF, and the complex then binds to platelet GPIb, resulting in
platelet agglutination.
CC -1- FUNCTION: There are two distinct forms of the von Willebrand
factor-dependent platelet coagglutinin. The dimeric form is
34-times more active than the one-chain Botrocetin in promoting
vWF binding to platelets.
CC -1- SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR PIR; B47267; B47267.
DR PDB; 1IJX; 17-JUL-02.
DR PDB; 1FVU; 14-FEB-01.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Lectin.
FT DISULFID 2 13
FT DISULFID 30 121
FT DISULFID 75 75 INTERCHAIN (WITH C-80 IN ALPHA CHAIN).

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FT DISULFID 98 113
SQ SEQUENCE 125 AA; 15037 MW; 1ED2027ED817FC0A CRC64;

Query Match
Best Local Similarity 73.1%; Score 79; DB 1; Length 125;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
    |||:|||||:|:|
Db 1 DCPDWSYEGHCYRVF 17

RESULT 9
ABAI TRIAB STANDARD; PRT; 131 AA.
AC P8111;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alboaggregin A subunit 1.
OS Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboaggregins A and B. Structure and interaction with human
RT platelets."
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
CC agglutination.
CC -1- SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
CC disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
DR HSP; P23806; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT_1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Lectin.
FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
FT DISULFID 2 13 BY SIMILARITY.
FT DISULFID 30 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
SQ SEQUENCE 131 AA; 15427 MW; B3569F5BF91F624 CRC64;

Query Match
Best Local Similarity 73.1%; Score 79; DB 1; Length 131;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
    |||:|||||:|:|
Db 1 DCPDWSYEGHCYRVF 17

RESULT 10
IXA TRIFL STANDARD; PRT; 152 AA.
AC P23806; Q91246;
DT 01-NOV-1991 (Rel. 20, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor IX/factor X-binding protein A chain precursor
DE (IX/X-BP).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OX OX Viperidae; Crotalinae; Trimeresurus.
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=96184662; PubMed=8645314;
RA RA Matsuzaki R., Yoshinara E., Yamada M., Shima K., Atoda H., Morita T.;
RT RT "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
RL RL protein from snake venom."
RN RN Biochem. Biophys. Res. Commun. 220:382-387(1996).
RP RP [2]
RC RC SEQUENCE OF 24-152.
RX RX TISSUE=Venom;
RA RA MEDLINE=91332000; PubMed=1831197;
RT RT Atoda H., Hyuga M., Morita T.;
RT RT "The primary structure of coagulation factor IX/factor X-binding
RT RT protein isolated from the venom of Trimeresurus flavoviridis.
RT RT Homology with asialoglycoprotein receptors, proteoglycan core
RT RT protein, tetranectin, and lymphocyte Fc epsilon receptor for
RT RT immunoglobulin E."
RN RN J. Biol. Chem. 266:14903-14911(1991).
RP RP [3]
RX RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RA RA MEDLINE=9731317; PubMed=9187649;
RT RT Mizuno H., Fujimoto Z., Koizumi M., Kano H., Atoda H., Morita T.;
RT RT "Structure of coagulation factors IX/X-binding protein, a heterodimer
RT RT of C-type lectin domains."
RN RN Nat. Struct. Biol. 4:438-441(1997).
CC CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND
CC CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.
CC CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL; D83331; BAAL1887.1; -.
DR DR PIR; JC4690; JC4690.
DR DR PDB; 1IXX; 06-MAY-98.
DR DR InterPro; IPR001304; Lectin_C.
DR DR InterPro; IPR003990; Pancreatis_ac.
DR DR Pfam; PF00059; lectin_c; 1.
DR DR PRINTS; PR01504; PNCREATITSAP.
DR DR SMART; SM00034; CLECT; 1.
DR DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW KW Lectin; Calcium; Signal; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 152 COAGULATION FACTOR IX/FACTOR X-BINDING
FT FT PROTEIN A CHAIN.
FT FT DOMAIN 24 152 C-TYPE LECTIN (LONG FORM).
FT FT DISULFID 25 36 BY SIMILARITY.
FT FT DISULFID 53 150 BY SIMILARITY.
FT FT DISULFID 102 102 INTERCHAIN (WITH C-98 OF B CHAIN).
FT FT DISULFID 125 142 BY SIMILARITY.
FT FT TURN 27 28
FT FT STRAND 30 31
FT FT STRAND 36 44
FT FT HELIX 46 56
FT FT TURN 58 59
FT FT STRAND 61 62
FT FT HELIX 68 81
FT FT STRAND 89 95
FT FT STRAND 105 105
FT FT TURN 107 108
FT FT STRAND 111 111

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FT STRAND 117 117
 FT HELIX 119 121
 FT STRAND 125 128
 FT HELIX 130 132
 FT TURN 133 134
 FT STRAND 137 140
 FT TURN 142 143
 FT STRAND 146 152
 SQ SEQUENCE 152 AA; 17213 MW; FB3DDDD2369009263 CRC64;

Query Match 70.4%; Score 76; DB 1; Length 152;
 Best Local Similarity 76.5%; Pred. No. 0.00029;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 24 DCLSGWSSYEGHCYKAF 40

RESULT 11

CVXB_CRODU STANDARD; PRT; 148 AA.
 AC O93427;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Convulxin beta precursor (CVX beta).
 OS Crotalus durissus terrificus (South American rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Crotalus.
 OC NCBI_TaxID=8732;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
 RC TISSUE=Venom gland;
 RA MEDLINE=98324901; PubMed=9657980;
 RX Leduc M., Bon C.;
 RT "Cloning of subunits of convulxin, a collagen-like platelet-
 aggregating protein from Crotalus durissus terrificus venom.";
 RL Biochem. J. 333:389-393(1998).
 CC -!- FUNCTION: Binds to the platelet and collagen receptor,
 Glycoprotein VI (GPVI).
 CC -!- SUBUNIT: Heterodimer of three alpha chains and three beta
 chains; disulfide-linked.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.

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DR EMBL; Y16349; CAA76182.1; -;
 DR HSSP; P23807; IIXX.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW Lectin; Glycoprotein; Signal.

FT SIGNAL 1 23
 FT CHAIN 24 148 CONVULXIN BETA.
 FT DOMAIN 34 145 C-TYPE LECTIN.
 FT DISULFID 26 26 INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT DISULFID 27 38 BY SIMILARITY.
 FT DISULFID 55 144 BY SIMILARITY.
 FT DISULFID 100 100 INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
 FT (POTENTIAL).
 FT DISULFID 121 136 BY SIMILARITY.
 SQ SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC693B9F CRC64;

Query Match 68.5%; Score 74; DB 1; Length 148;
 Best Local Similarity 68.8%; Pred. No. 0.00054;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CDPSEWSSYEGFCYKPF 17
 ||| ||||| :|||
 Db 27 CDPHSSYDRYCYKVF 42

RESULT 12

RHCA_AGRKH STANDARD; PRT; 133 AA.
 AC P81397;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Rhodocetin alpha subunit.
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Calloselasma.
 OC NCBI_TaxID=8717;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RA MEDLINE=99303998; PubMed=10360956;
 RX Wang R., Kini R.M., Chung M.C.M.;
 RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
 Calloselasma rhodostoma (Malayan pit viper): synergistic and
 noncovalent interaction between its subunits.";
 RL Biochemistry 38:7584-7593(1999).
 CC -!- FUNCTION: A potent inhibitor of collagen-induced platelet
 aggregation. Individually, neither subunit inhibits platelet
 aggregation. Both subunits are essential.
 CC -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
 together by noncovalent interactions rather than by intersubunit
 disulfide bridges.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; IIXX.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE NEG.
 DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 133 AA; 15962 MW; 386EAC519DFC674D CRC64;

Query Match 66.7%; Score 72; DB 1; Length 133;
 Best Local Similarity 58.8%; Pred. No. 0.00095;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| :|||
 Db 1 DCPDGSSTKSYCYRPF 17

RESULT 13

ABBA_TRIAB STANDARD; PRT; 132 AA.
 ID ABBA_TRIAB
 AC P81115;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alboaggregin B alpha subunit.
 OS Trimeresurus albolabris (White-lipped pit viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Trimeresurus.
 RN NCBI_TaxID=8765;
 EN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=98189535; PubMed=9531050;
 RA Kowalek M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
 RA Calvete J.J., Niewiarowski S.;
 RT "Alboaggregins A and B. Structure and interaction with human
 RT platelets.";
 RL Thromb. Haemost. 79:609-613(1998).
 CC -!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits, disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 127 BY SIMILARITY.
 FT DISULFID 79 79 INTERCHAIN (WITH C-75 IN BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 102 119 BY SIMILARITY.
 SQ SEQUENCE 132 AA; 15419 MW; 6FAE64820383F16F CRC64;
 Query Match 63.9%; Score 69; DB 1; Length 132;
 Best Local Similarity 60.0%; Pred. No. 0.0026;
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYK 15
 DB 1 DCPDWSWSSFKQCYQ 15
 RESULT 14
 ECHB_ECHCA
 ID ECHB_ECHCA STANDARD; PRT; 123 AA.
 AC P81996;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Echicetin beta subunit.
 OS Echis carinatus (Saw-scaled viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Echis.
 OX NCBI_TaxID=40353;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=95091801; PubMed=7999097;
 RA Peng M., Holt J.C., Niewiarowski S.;
 RT "Isolation, characterization and amino acid sequence of echicetin beta
 RT subunit, a specific inhibitor of von Willebrand factor and thrombin
 RT interaction with glycoprotein Ib.";
 RL Biochem. Biophys. Res. Commun. 205:68-72(1994).
 CC [2]
 CC SEQUENCE OF 1-30.
 CC TISSUE=Venom;
 RX MEDLINE=97250657; PubMed=9163349;
 RA Polgar J., Magnat E.M., Peitsch M.C., Wells T.N.C., Saqi M.S.A.,
 RA Clemetson K.J.;
 RT "Amino acid sequence of the alpha subunit and computer modelling of
 RT the alpha and beta subunits of echicetin from the venom of Echis
 RT carinatus (saw-scaled viper).";
 RL Biochem. J. 323:533-537(1997).

RN [3]
 RP CHARACTERIZATION.
 RC TISSUE=Venom;
 RX MEDLINE=93244424; PubMed=8481512;
 RA Peng M., Lu W., Bevilacqua L., Niewiarowski S., Kirby E.P.;
 RT "Echicetin: a snake venom protein that inhibits binding of von
 RT Willebrand factor and alboaaggregins to platelet glycoprotein Ib.";
 RL Blood 81:2321-2328(1993).
 CC -!- FUNCTION: Binds to platelet GPIb and inhibits platelet
 CC agglutination.
 CC -!- SUBUNIT: Heterodimer of alpha and beta subunits.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23807; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 2 13 BY SIMILARITY.
 FT DISULFID 30 119 BY SIMILARITY.
 FT DISULFID 75 75 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY
 FT SIMILARITY).
 FT DISULFID 96 111 BY SIMILARITY.
 SQ SEQUENCE 123 AA; 14869 MW; C42C0AD7CDE18CA6 CRC64;
 Query Match 62.0%; Score 67; DB 1; Length 123;
 Best Local Similarity 58.8%; Pred. No. 0.0047;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DCPSEWSSYEGFCYKPF 17
 DB 1 NCLPDWSVYEGCYKVF 17
 RESULT 15
 RHCB_AGRKH
 ID RHCB_AGRKH STANDARD; PRT; 129 AA.
 AC P81398;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Rhodocetin beta subunit.
 OS Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Calloselasma.
 OX NCBI_TaxID=8717;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=9303998; PubMed=10360956;
 RA Wang R., Kini R.M., Chung M.C.M.;
 RT "Rhodocetin, a novel platelet aggregation inhibitor from the venom of
 RT Calloselasma rhodostoma (Malayan pit viper): synergistic and
 RT noncovalent interaction between its subunits.";
 RL Biochemistry 38:7584-7593(1999).
 CC -!- FUNCTION: A potent inhibitor of collagen-induced platelet
 CC aggregation. Individually, neither subunit inhibits platelet
 CC aggregation. Both subunits are essential.
 CC -!- SUBUNIT: Heterodimer of one alpha and one beta subunit held
 CC together by noncovalent interactions rather than by intersubunit
 CC disulfide bridges.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=15184.53; MW_ERR=2.74; METHOD=Electrospray.
 CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
 DR HSSP; P23806; 11XX.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C-TYPE LECTIN 1; FALSE-NEG.
 KW LECTIN; PS00041; C-TYPE LECTIN_2; 1.
 FT DOMAIN 3 125 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 4 15 BY SIMILARITY.
 FT DISULFID 98 115 BY SIMILARITY.
 SQ SEQUENCE 129 AA; 15190 MW; EF4B318FAAC807AE CRC64;
 Query Match 59.3%; Score 64; DB 1; Length 129;
 Best Local Similarity 56.2%; Pred. NO. 0.013;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CFEWSYEGFCYKPF 17
 ||: ||: : |||||
 Db 4 CFTWSASKLYCYKPF 19

Search completed: December 8, 2003, 09:53:10
 Job time : 2.56762 secs

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OM protein - protein search, using sw model

Run on: December 8, 2003, 09:49:24 ; Search time 8.25714 Seconds
(without alignments)
531.285 Million cell updates/sec.

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mic:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	101	93.5	146	13 Q8JIW1	Q8jiw1 agkistrodon
2	98	90.7	124	13 Q98SM5	Q98sm5 agkistrodon
3	98	90.7	146	13 Q9IAM1	Q9iam1 agkistrodon
4	98	90.7	146	13 Q9DEF8	Q9def8 agkistrodon
5	98	90.7	146	13 Q9JIV7	Q9jiv7 agkistrodon
6	94	87.0	146	13 Q9DG31	Q9dg31 agkistrodon
7	94	87.0	146	13 Q9I840	Q9i840 agkistrodon
8	93	85.1	146	13 Q8AY84	Q8aya8 agkistrodon
9	86	79.6	146	13 Q9YI92	Q9yi92 agkistrodon
10	84	77.8	145	13 Q9PS05	Q9ps05 bothrops ja
11	84	77.8	145	13 Q9YGN4	Q9ygn4 agkistrodon
12	81	75.0	30	13 Q9PS06	Q9ps06 bothrops ja
13	80	74.1	152	13 Q9DEF9	Q9def9 agkistrodon
14	80	74.1	152	13 Q8JIW0	Q8jiw0 agkistrodon
15	79	73.1	152	13 Q9DG39	Q9dg39 agkistrodon
16	78	72.2	124	13 Q90WL9	Q90wl9 agkistrodon

17	78	72.2	155	13 Q8JIV8	Q8jiv8 agkistrodon
18	77	71.3	40	13 Q9PS20	Q9ps20 trimeresuru
19	77	71.3	152	13 Q9IAM1	Q9iam1 agkistrodon
20	76	70.4	33	13 Q9PRQ7	Q9prq7 bothrops ja
21	76	70.4	123	13 Q9PSM5	Q9psm5 bothrops ja
22	76	70.4	146	13 Q98UJ0	Q98uj0 trimeresuru
23	73	67.6	146	13 Q9DEA1	Q9dea1 agkistrodon
24	71	65.7	157	13 Q9YGG9	Q9ygg9 agkistrodon
25	69	63.9	40	13 Q9PS19	Q9ps19 trimeresuru
26	66	61.1	42	13 Q9PRQ8	Q9prq8 bothrops ja
27	66	61.1	142	13 Q9PSM6	Q9psm6 bothrops ja
28	66	61.1	149	13 Q8UVC7	Q8uvc7 agkistrodon
29	66	61.1	149	13 Q8AYA3	Q8aya3 agkistrodon
30	66	61.1	151	13 Q8JIW2	Q8jiw2 agkistrodon
31	66	61.1	155	13 Q9DEA2	Q9dea2 agkistrodon
32	65	60.2	30	13 Q9PRP8	Q9prp8 echis carin
33	65	60.2	131	13 Q9PSM9	Q9psm9 echis carin
34	62	57.4	1152	13 Q90WM2	Q90wm2 xenopus lae
35	61	56.5	155	13 Q8JIV6	Q8jiv6 agkistrodon
36	60	55.6	30	13 Q9PRP7	Q9prp7 echis carin
37	58	53.7	16	13 Q9PRZ4	Q9prz4 bothrops ja
38	58	53.7	37	13 Q9PRT1	Q9prt1 trimeresuru
39	58	53.7	146	13 Q8JGT6	Q8jgt6 trimeresuru
40	58	53.7	148	13 Q8AV98	Q8av98 trimeresuru
41	58	53.7	149	5 Q02582	Q02582 inciliaria f
42	58	53.7	154	13 Q9YGN5	Q9ygn5 agkistrodon
43	57	52.8	34	13 Q9PRT2	Q9prt2 trimeresuru
44	57	52.8	158	13 Q8UVC6	Q8uvc6 agkistrodon
45	57	52.8	158	13 Q8JGT7	Q8jgt7 trimeresuru

ALIGNMENTS

RESULT 1

Q8JIW1 ID Q8JIW1 PRELIMINARY; PRT; 146 AA.
AC Q8JIW1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Agkisacutacin B-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Deinagkistrodon.
CX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RT "B chain of agkisacutacin from Deinagkistrodon acutus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091756; AAM22785.1; -
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatiss_ac.
DR Pfam; PF00059; lectin; C; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 146 AA; 16740 MW; 626086D68741317C CRC64;

Query Match 93.5%; Score 101; DB 13; Length 146;

Best Local Similarity 94.1%; Pred. No. 9.3e-08;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCPSEWSYEGFCYKPF 17

Db 24 DCPSEWSYEGHCYKPF 40

RESULT 2

Q98SM5

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ID Q98SM5 PRELIMINARY; PRT; 124 AA.
AC Q98SM5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Agkisacin-b.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Zha X., Xu K.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF350324; RAK26430.1; -.
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 124 AA; 14701 MW; 4682DSE0CB3DC518 CRC64;

Query Match 90.7%; Score 98; DB 13; Length 124;
Best Local Similarity 88.2%; Pred. No. 2.3e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 2 DCPSDWSYEGHCYKPF 18

RESULT 3
Q91AM0 PRELIMINARY; PRT; 146 AA.
ID Q91AM0;
AC Q91AM0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Agkisacutacin B chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
RA Liu J.;
RL "Agkisacutacin, a new fibrinolytic & anti-platelet protein from
Agkistrodon acutus venom.";
DR EMBL; AF176421; AAF26287.1; -.
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pncreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16726 MW; 7360B6D6864131B8 CRC64;

Query Match 90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 24 DCPSDWSYEGHCYKPF 40

RESULT 4
Q9DEF8 PRELIMINARY; PRT; 146 AA.
ID Q9DEF8;
AC Q9DEF8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Anticoagulant protein-B precursor.
GN ACP-B.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Tani A., Nose T., Nikandrov N.N., Ogawa T., Deshimaru M., Fukumaki Y.,
RA Chang C., Shimohigashi Y., Ohno M.;
RL "Purification, sequencing, and cDNA cloning of a heterodimeric
anticoagulant protein from Deinagkistrodon actus venom gland.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036881; BAB20441.1; -.
DR HSP; P23807; IIXX.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pncreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 146 AA; 16997 MW; 420D71EBB4E9F5D2 CRC64;

Query Match 90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DCPSEWSYEGFCYKPF 17
Db 24 DCPSDWSYEGHCYKPF 40

RESULT 5
Q8JIV7 PRELIMINARY; PRT; 146 AA.
ID Q8JIV7;
AC Q8JIV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ACF 1/2 B-chain.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu H., Xiang K., Wang Y., Liu J.;
RL "B chain of ACF 1/2 from Deinagkistrodon acutus.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY091761; AAM22789.1; -.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pncreatis_ac.
DR Pfam; PF00059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16925 MW; F2493CACBA5D2144 CRC64;

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Query Match      90.7%; Score 98; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 2.7e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPSEWSSVEGHCYKPF 40

RESULT 6
QSDG31
ID Q9DG31 PRELIMINARY; PRT; 146 AA.
AC Q9DG31;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Halysin B-chain precursor.
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Venom;
RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
RT "A Novel Coagulation Factor Xa Inhibitor from Korean Snake (Agkistrodon halys) venom.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF197915; AAG28522.1; -.
DR HSSP; P23807; 11XX.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c.1.
DR PRINTS; PR01504; PNCEAITSAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;

Query Match      87.0%; Score 94; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPSEWSSVEGHCYKPF 40

RESULT 8
Q8AYA4
ID Q8AYA4 PRELIMINARY; PRT; 146 AA.
AC Q8AYA4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Agglucetin-beta 1 subunit precursor.
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
OX NCBI_TaxID=36307;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21542539; PubMed=11686327;
RA Wang W.-J., Huang T.F.;
RT "A novel tetrameric venom protein, agglucetin from Agkistrodon acutus, acts as a glycoprotein Ib agonist.";
RL Thromb. Haemost. 86:1077-1086(2001).
RN [2];
RP SEQUENCE FROM N.A.
RA Wang W.-J., Ling Q.-D., Huang T.-F.;
RT "Molecular structure and functional characterization of agglucetin, a tetrameric glycoprotein Ib-binding protein, from Formosan pit viper.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF540647; AAN23126.1; -.
KW Signal.
FT SIGNAL.
FT CHAIN 24 146 AGGLUCETIN-BETA 1 SUBUNIT.
SQ SEQUENCE 146 AA; 16728 MW; 2342BAE39EBOCCB9 CRC64;

Query Match      86.1%; Score 93; DB 13; Length 146;
Best Local Similarity 88.2%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSVEGFCYKPF 17
DB 24 DCPSEWSSVEGHCYKPF 40

RESULT 9
Q9YI92
ID Q9YI92 PRELIMINARY; PRT; 146 AA.
AC Q9YI92;

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DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Mamushigin beta.
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Agkistrodon.
 OX NCBI_TaxID=61300;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98319530; PubMed=9657448;
 RA Sakurai Y., Fujimura Y., Kokubo T., Inamura K., Kawasaki T., Handa M.,
 RA Suzuki M., Matsui T., Titani K., Yoshioka A.,
 RT "The cDNA cloning and molecular characterization of a snake venom
 RT platelet glycoprotein IB-binding protein, mamushigin, from Agkistrodon
 RT halys blomhoffii venom.";
 RL Thromb. Haemost. 79:1199-1207(1998).
 DR EMBL; AB019616; BAA34425.1; -
 DR HSP; P23807; IXX.
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 146 AA; 17064 MW; 3EDA84BDC24E76D CRC64;

Query Match 79.6%; Score 86; DB 13; Length 146;
 Best Local Similarity 76.5%; Pred. No. 1.7e-05;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 |||||:|||||:|
 Db 24 DCPSEWSSYEGHCYRVF 40

RESULT 10

Q9PS05 PRELIMINARY; PRT; 30 AA.
 AC Q9PS05;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Factor IX/factor X-binding protein A chain (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93326575; PubMed=8334120;
 RA Sekiya F., Atoda H., Morita T.;
 RT "Isolation and characterization of an anticoagulant protein homologous
 RT to botrocetin from the venom of Bothrops jararaca.";
 RL Biochemistry 32:6892-6897(1993).
 DR HSP; P23807; IXX.
 SQ SEQUENCE 30 AA; 3709 MW; DD49A218EDDBA9D2 CRC64;

Query Match 77.8%; Score 84; DB 13; Length 30;
 Best Local Similarity 76.5%; Pred. No. 7.7e-06;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 |||||:|||||:|
 Db 1 DCPSEWSSYEGHCYRVF 17

RESULT 11

Q9YGN4 PRELIMINARY; PRT; 145 AA.
 ID Q9YGN4;
 AC Q9YGN4;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibrinogen clotting inhibitor B chain.
 OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
 OS brevicaudus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Agkistrodon.
 OX NCBI_TaxID=66175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim D.S., Koh Y.S.;
 RT "Purification and molecular cloning of snake venom fibrin clotting
 RT inhibitor.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF125310; AAD18056.1; -
 DR HSP; P23807; IXX.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR003990; Pancreatis_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
 SQ SEQUENCE 145 AA; 16746 MW; 6FFC67E2C1F20BC8 CRC64;

Query Match 77.8%; Score 84; DB 13; Length 145;
 Best Local Similarity 82.4%; Pred. No. 3.5e-05;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 |||||:|||||:|
 Db 24 DCPSEWSSYEGHCYRVF 40

RESULT 12

Q9PS06 PRELIMINARY; PRT; 30 AA.
 AC Q9PS06;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Factor IX/factor X-binding protein B chain (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93326575; PubMed=8334120;
 RA Sekiya F., Atoda H., Morita T.;
 RT "Isolation and characterization of an anticoagulant protein homologous
 RT to botrocetin from the venom of Bothrops jararaca.";
 RL Biochemistry 32:6892-6897(1993).
 DR HSP; P23807; IXX.
 SQ SEQUENCE 30 AA; 3506 MW; 14A2DFFB41F2B6F5 CRC64;

Query Match 75.0%; Score 81; DB 13; Length 30;
 Best Local Similarity 70.6%; Pred. No. 2.2e-05;

Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DCPSEWSSYEGFCYKPF 17
 |||||:|||||:|
 Db 1 DCPSEWSSYEGHCYRVF 17

RESULT 13

Q9DEF9 PRELIMINARY; PRT; 152 AA.
 ID Q9DEF9;
 AC Q9DEF9;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anticoagulant protein A precursor.
 GN ACP-A.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 GN NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RA Ogawa T., Tani A.;
 RT "Purification, Sequencing, and cDNA Cloning of a Heterodimeric
 RL Anticoagulant Protein from Agkistrodon actus Venom Gland.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB036880; BAA99281.1; -;
 DR HSSP; P23806; IIXX.
 DR InterPro; IPR001304; LECTIN_C.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 152 AA; 17124 MW; 5C59C0F503A4D223 CRC64;

Query Match 74.1%; Score 80; DB 13; Length 152;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 24 DCSSSWSSYEGHCYKAF 40

RESULT 14

ID Q8JIW0 PRELIMINARY; PRT; 152 AA.
 AC Q8JIW0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ACF 1/2 A-chain.
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Deinagkistrodon.
 OX NCBI_TaxID=36307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yu H., Xiang K., Wang Y., Liu J.;
 RT "A chain of ACF 1/2 from Deinagkistrodon acutus.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY091758; AAM22786.1; -;
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR003990; Pancreatins_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 SQ SEQUENCE 152 AA; 17108 MW; B0870F3DA0A4D23B CRC64;

Query Match 74.1%; Score 80; DB 13; Length 152;
 Best Local Similarity 76.5%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 24 DCSSSWSSYEGHCYKAF 40

RESULT 15

Q9DG39 PRELIMINARY; PRT; 152 AA.
 AC Q9DG39;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Halysin A-chain precursor.
 GN HXNA.
 OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;
 RT "A novel coagulation factor Xa inhibitor from Korean snake
 RL (Agkistrodon halys) venom.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF190827; AAGL7178.1; -;
 DR HSSP; P23806; IIXX.
 DR InterPro; IPR001304; LECTIN_C.
 DR InterPro; IPR003990; Pancreatins_ac.
 DR Pfam; PF00059; lectin_c; 1.
 DR PRINTS; PR01504; PNCREATITSAP.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 152 AA; 17455 MW; BDD74D1DC280C28D CRC64;

Query Match 73.1%; Score 79; DB 13; Length 152;
 Best Local Similarity 76.5%; Pred. No. 0.00021;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DCPSEWSSYEGFCYKPF 17
 ||| ||||| |||||
 Db 24 DCPSEWSSYEGHCYNIF 40

Search completed: December 8, 2003, 09:54:48
 Job time : 8.25714 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 8, 2003, 13:34:19 ; Search time 440.543 Seconds
(without alignments)
937.879 Million cell updates/sec

Title: US-09-938-114-4
Perfect score: 108
Sequence: 1 DCPSEWSYEGFCYKPF 17

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

EST :

1: em estba:*
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5: em estov:*
6: em estpl:*
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10: gb est2:*
11: gb htc:*
12: gb est3:*
13: gb est4:*
14: gb est5:*
15: em estfun:*
16: em estom:*
17: em gss_hum:*
18: em gss_inv:*
19: em gss_pln:*
20: em gss_vrt:*
21: em gss_fun:*
22: em gss_mam:*
23: em gss_mus:*
24: em gss_pro:*
25: em gss_rod:*
26: em gss_phg:*
27: em gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	76.9	172	12	BM401696 PH1A01F S
2	83	76.9	343	12	BM401656 PH1E04F S
3	83	76.9	378	12	BM401618 J11C07F S
4	83	76.9	391	12	BM401469 JH1B09F S
5	83	76.9	475	12	BM401621 J11D02F S
6	83	76.9	504	12	BM401628 J11E12F S
7	83	76.9	510	12	BM401667 J12H07F S
8	83	76.9	512	12	BM401495 JH2B09F S
9	82	75.9	374	12	BM401520 JH2G02F S
10	82	75.9	497	12	BM401552 JH3E12F S
11	80	74.1	378	12	BM401620 J11C11F S
12	80	74.1	460	12	BM401460 JH1D06F S
13	80	74.1	574	12	BM401417 GH061F Sn
14	80	74.1	654	12	BM401401 GH025F Sn
15	76	70.4	633	12	BM401686 PH015FB S
16	67	62.0	184	12	BM401646 J12A05F S
17	66	61.1	298	12	BM401455 JH1C07F S
18	66	61.1	307	12	BM401567 JH4A07F S
19	66	61.1	315	12	BM401503 JH2D02F S
20	66	61.1	321	12	BM401611 J11B01F S
21	66	61.1	388	12	BM401625 J11E05F S
22	66	61.1	401	12	BM401610 J11A11F S
23	66	61.1	405	12	BM401607 JH4H07F S
24	66	61.1	410	12	BM401605 JH4H07F S
25	66	61.1	440	12	BM401459 JH1D05F S
26	66	61.1	440	12	BM401637 J11G11F S
27	66	61.1	453	12	BM401653 J12D01F S
28	66	61.1	458	12	BM401641 J11H06F S
29	66	61.1	501	12	BM401648 J12B03F S
30	66	61.1	511	12	BM401631 J11F11F S
31	66	61.1	556	12	BM401668 J12H08F S
32	65	60.2	200	12	BM401669 J12H09F S
33	65	60.2	365	12	BM401665 J12H01F S
34	65	60.2	456	12	BM401659 J12F01F S
35	62	57.4	318	9	AI724077 RH1Z1 26
36	62	57.4	522	9	AI724149 RH1Z1 7 E
37	62	57.4	533	13	BQ656090 PRC1061 S
38	62	57.4	533	13	BQ656093 PRC1065 S
39	61	56.5	556	9	AA618477 mm09a06.s
40	61	56.5	589	10	AW945357 PM3-EN000
41	61	56.5	595	10	BE825502 PM3-EN000
42	61	56.5	598	13	BU323232 603490804
43	61	56.5	702	13	BU266055 603815327
44	61	56.5	703	13	BU269611 603816223
45	61	56.5	726	13	BU230613 603399651

ALIGNMENTS

RESULT 1
BM401696 172 bp mRNA linear EST 01-MAY-2002
LOCUS PH1A01F Snake Bothrops insularis library IL2 Bothrops insularis
DEFINITION cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION BM401696
VERSION BM401696.1 GI:20376324
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Lepidosaoria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 172)
 AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake *Bothrops insularis* through the generation of expressed sequence tags (ESTs)
 JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..172
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL2"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 34 a 39 c 47 g 42 t 10 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00326 Length: 172
 Score: 83.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401696 (1-172)
 Qy 1 AspCysProSerGluTyrSerSerTyrgluGlyPheCysTyrLysProPhe 17
 Db 82 GATTGTCCCTGATTGGTCCCTATGAGGGGCAATGCTACAGCTCTTC 132

RESULT 2
 BM401656
 LOCUS
 DEFINITION J12E04F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCSSION BM401656
 VERSION BM401656.1 GI:20376284
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 1 (bases 1 to 343)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of the pitviper snake *Bothrops insularis* through the generation of expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 JOURNAL 2247338
 MEDLINE

12459276
 COMMENT Contact: Paulo Lee Ho
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 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES
 source
 Location/Qualifiers
 1..343
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco RI; Site 2: Not I; 5'ug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."

BASE COUNT 79 a 83 c 90 g 86 t 5 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.00845 Length: 343
 Score: 83.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401656 (1-343)
 Qy 1 AspCysProSerGluTyrSerSerTyrgluGlyPheCysTyrLysProPhe 17
 Db 131 GATTGTCCCTGATTGGTCCCTATGAGGGGCAATGCTACAGCTCTTC 181

RESULT 3
 BM401618
 LOCUS
 DEFINITION J11C07F Snake Bothrops insularis library IL3 Bothrops insularis cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
 ACCSSION BM401618
 VERSION BM401618.1 GI:20376246
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Bothrops insularis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
 1 (bases 1 to 378)
 Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 A survey of gene expression and diversity in the venom glands of the pitviper snake *Bothrops insularis* through the generation of expressed sequence tags (ESTs)
 Gene 299 (1-2), 279-291 (2002)
 JOURNAL 22347338
 MEDLINE 12459276
 PUBMED
 COMMENT Contact: Paulo Lee Ho
 Centro de Biotecnologia
 Instituto Butantan
 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505

Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13P.
Location/Qualifiers

FEATURES

source

```
1. .378
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco
RI; Site 2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
```

BASE COUNT 88 a 91 c 102 g 95 t 2 others

ORIGIN

```
Alignment Scores:
Pred. No.: 0.00967 Length: 378
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0
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US-09-938-114-4 (1-17) x BM401618 (1-378)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
Db 78 GATTGTCCTCTGATTGTCCTATGAGGCGCATTCGCTACAGCTCTTC 128

RESULT 4

BM401469

LOCUS

DEFINITION JH1E09F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

BM401469

VERSION

BM401469.1

KEYWORDS

GI:20376097

SOURCE

ORGANISM

Bothrops insularis (island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 391)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED

12459276

COMMENT

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Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL03A (see Reference)

Seq primer: M13P.

Location/Qualifiers

1. .391

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco

RI; Site 2: Not I; Sug of mRNA from Bothrops insularis

venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (Life Technologies). The cDNAs

were selected by size (350-600 pb and up 600 pb) in

agarose gel electrophoresis, linked to Eco RI adapters and

directionally cloned in pGEM11zf+ vector (Promega). ESTs

were generated from random clones and grouped in unique

sequences. The putative identification of each EST or

cluster was obtained through Blast searches (e-value <

e-05)."

BASE COUNT 91 a 92 c 113 g 95 t

ORIGIN

Alignment Scores:

```
Pred. No.: 0.0101 Length: 391
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0
```

US-09-938-114-4 (1-17) x BM401469 (1-391)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17

Db 135 GATTGTCCTCTGATTGTCCTATGAGGCGCATTCGCTACAGCTCTTC 185

RESULT 5

BM401621

LOCUS

JH1D02F Snake Bothrops insularis library IL3 Bothrops insularis

cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION

BM401621

VERSION

BM401621.1

KEYWORDS

GI:20376249

SOURCE

ORGANISM

Bothrops insularis (island jararaca)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

Viperidae; Crotalinae; Bothrops.

1 (bases 1 to 475)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

A survey of gene expression and diversity in the venom glands of

the pitviper snake Bothrops insularis through the generation of

expressed sequence tags (ESTs)

Gene 299 (1-2), 279-291 (2002)

22347338

PUBMED

12459276

COMMENT

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Tel: 55 11 37 26 7222 ext. 2083

Fax: 55 11 37 26 1505

Email: hoplee@usp.br

This EST corresponds to cluster BITL01A (see Reference)

Seq primer: M13P.

Location/Qualifiers

1. .475

/organism="Bothrops insularis"

/mol_type="mRNA"

/db_xref="taxon:8723"

/tissue_type="venom glands"

/clone_lib="Snake Bothrops insularis library IL3"

/note="Organ: venom glands; Vector: pGEM11zf+; Site 1: Eco

RI; Site 2: Not I; Sug of mRNA from Bothrops insularis

venom glands were primed with oligo-(dT) and reverse

transcribed to cDNA using Superscript Plasmid System for

cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05).

BASE COUNT 113 a 111 c 133 g 117 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 0.0133 Length: 475
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401621 (1-475)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||
129 GATTGTCCTCTGATTGGTCCCTATGAGGCGATTGCTACAGCTCTTC 179

RESULT 6

BM401628

LOCUS BM401628 504 bp mRNA linear EST 01-MAY-2002
DEFINITION JLI12F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401628

VERSION BM401628.1 GI:20376256

KEYWORDS EST.

SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 504)

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE 22347338

PUBMED 12459276

COMMENT Contact: Paulo Lee Ho
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13F.

FEATURES

source

Location/Qualifiers
1..504
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <

e-05)."
BASE COUNT 128 a 113 c 140 g 120 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 0.0144 Length: 504
Score: 83.00 Matches: 13
Percent Similarity: 82.35% Conservative: 1
Best Local Similarity: 76.47% Mismatches: 3
Query Match: 76.85% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401628 (1-504)

Qy 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProphe 17
|||||
96 GATTGTCCTCTGATTGGTCCCTATGAGGCGATTGCTACAGCTCTTC 146

RESULT 7

BM401667

LOCUS BM401667 510 bp mRNA linear EST 01-MAY-2002
DEFINITION JLI2H07F Snake Bothrops insularis library IL3 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.

ACCESSION BM401667

VERSION BM401667.1 GI:20376295

KEYWORDS EST.

SOURCE Bothrops insularis (island jararaca)

ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 510)

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.

TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)

JOURNAL Gene 299 (1-2), 279-291 (2002)

MEDLINE 22347338

PUBMED 12459276

COMMENT Contact: Paulo Lee Ho
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Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL01A (see Reference)
Seq primer: M13F.

FEATURES

source

Location/Qualifiers
1..510
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue type="venom glands"
/clone lib="Snake Bothrops insularis library IL3"
/note="Organ: venom glands; Vector: pGEM11zf+; Site: 1: Eco RI; Site 2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value <

BASE COUNT 128 a 117 c 141 g 121 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 0.0146 Length: 510
Score: 83.00 Matches: 13

Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401667 (1-510)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
 DB 93 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAGCTCTTC 143

RESULT 8

BM401495 512 bp mRNA linear EST 01-MAY-2002
 LOCUS JH2809F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION CDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401495
 VERSION BM401495.1 GI:20376123
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 512)

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
 JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276

COMMENT Contact: Paulo Lee Ho
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 Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL01A (see Reference)
 Seq primer: M13F.

FEATURES

Source Location/Qualifiers
 1..512
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site.1: Eco RI; Site.2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript plasmid system for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adaptors and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
 BASE COUNT 129 a 116 c 143 g 119 t 5 others
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0147 Length: 512
 Score: 83.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 76.85% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401495 (1-512)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
 DB 99 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAGCTCTTC 149

RESULT 9

BM401520 374 bp mRNA linear EST 01-MAY-2002
 LOCUS JH2802F Snake Bothrops insularis library IL3 Bothrops insularis
 DEFINITION CDNA 5', similar to Snake venom C-type lectin, mRNA sequence.
 ACCESSION BM401520
 VERSION BM401520.1 GI:20376148
 KEYWORDS EST.
 SOURCE Bothrops insularis (island jararaca)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 Viperidae; Crotalinae; Bothrops.

REFERENCE 1 (bases 1 to 374)

AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
 TITLE A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tags (ESTs)
 JOURNAL Gene 299 (1-2), 279-291 (2002)
 MEDLINE 22347338
 PUBMED 12459276

COMMENT Contact: Paulo Lee Ho
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 Tel: 55 11 37 26 7222 ext. 2083
 Fax: 55 11 37 26 1505
 Email: hoplee@usp.br
 This EST corresponds to cluster BITL06A (see Reference)
 Seq primer: M13F.

FEATURES

Source Location/Qualifiers
 1..374
 /organism="Bothrops insularis"
 /mol_type="mRNA"
 /db_xref="taxon:8723"
 /tissue_type="venom glands"
 /clone_lib="Snake Bothrops insularis library IL3"
 /note="Organ: venom glands; Vector: pGEM11zf+; Site.1: Eco RI; Site.2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript plasmid system for cDNA Synthesis and Cloning (Life Technologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adaptors and directionally cloned in pGEM11zf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
 BASE COUNT 83 a 83 c 114 g 94 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0135 Length: 374
 Score: 82.00 Matches: 13
 Percent Similarity: 82.35% Conservative: 1
 Best Local Similarity: 76.47% Mismatches: 3
 Query Match: 75.93% Indels: 0
 DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401520 (1-374)

QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrIlysProPhe 17
 DB 130 GATTGTCCTCTGATTGGTCCCTATGAAGGCGATTGCTACAAGCTCTTC 180

RESULT 10

BM401552 497 bp mRNA linear EST 01-MAY-2002
 LOCUS


```

source
1. .654
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco
RI; Site:2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
BASE COUNT 154 a 156 c 175 g 161 t 8 others
ORIGIN
Alignment Scores:
Pred. No.: 0.0587 Length: 654
Score: 80.00 Matches: 12
Percent Similarity: 82.35% Conservative: 2
Best Local Similarity: 70.59% Mismatches: 3
Query Match: 74.07% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401401 (1-654)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 143 GATTGTCCTCTGATTGTCCTCTCTGATGAGGGAGTGTCTACAGGGCTTTC 193

RESULT 15
BM401686
LOCUS
DEFINITION PH015FB Snake Bothrops insularis library IL2 Bothrops insularis
cDNA 5' similar to Snake venom C-type lectin, mRNA sequence.
ACCESSION BM401686
VERSION BM401686.1 GI:20376314
KEYWORDS EST.
SOURCE Bothrops insularis (island jararaca)
ORGANISM Bothrops insularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
REFERENCE 1 (bases 1 to 633)
AUTHORS Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
TITLE A survey of gene expression and diversity in the venom glands of
the pitviper snake Bothrops insularis through the generation of
expressed sequence tags (ESTs)
JOURNAL Gene 299 (1-2), 279-291 (2002)
MEDLINE 22347338
PUBMED 12459276
COMMENT Contact: Paulo Lee Ho
Centro de Biotecnologia
Instituto Butantan
Av. Vital Brazil, 1500, Sao Paulo SP, BRAZIL, 05503-900
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
Email: hoplee@usp.br
This EST corresponds to cluster BITL02A (see Reference)
Seq primer: M13F.
Location/Qualifiers
1. .633
/organism="Bothrops insularis"
/mol_type="mRNA"
/db_xref="taxon:8723"
/tissue_type="venom glands"
/clone_lib="Snake Bothrops insularis library IL2"
/notes="Organ: venom glands; Vector: pGEM11zf+; Site:1: Eco
RI; Site:2: Not I; Sug of mRNA from Bothrops insularis
venom glands were primed with oligo-(dT) and reverse
transcribed to cDNA using Superscript Plasmid System for
cDNA Synthesis and Cloning (Life Technologies). The cDNAs
were selected by size (350-600 pb and up 600 pb) in
agarose gel electrophoresis, linked to Eco RI adapters and
directionally cloned in pGEM11zf+ vector (Promega). ESTs
were generated from random clones and grouped in unique
sequences. The putative identification of each EST or
cluster was obtained through Blast searches (e-value <
e-05)."
BASE COUNT 145 a 148 c 155 g 171 t 14 others
ORIGIN
Alignment Scores:
Pred. No.: 0.226 Length: 633
Score: 76.00 Matches: 12
Percent Similarity: 76.47% Conservative: 1
Best Local Similarity: 70.59% Mismatches: 4
Query Match: 70.37% Indels: 0
DB: 12 Gaps: 0

US-09-938-114-4 (1-17) x BM401686 (1-633)
QY 1 AspCysProSerGluTrpSerSerTyrGluGlyPheCysTyrLysProPhe 17
DB 82 GATTGTCCTCTGATTGTCCTCTCTGATGAGGGAGTGTCTACAGGGCTTTC 132

Search completed: December 8, 2003, 17:24:34
Job time : 441.543 secs

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